

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 1

TO: Jennifer Graser

Location: REM/3B09/3C18

Art Unit: 1645
June 7, 2004

Case Serial Number: 10/712713

From: P. Sheppard

Location: Remsen Building

Phone: (571) 272-2529

sheppard@uspto.gov

Search Notes	

ADDRESSEE: Human

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SOFTWARE: ASCII Text
                                                                                                                                    CURRENT APPLICATION DATA:
                                                   ZIP: 20850
COMPUTER READABLE FORM
STREET: 9410 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
               CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Matches 1314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craig A. Rosen Steven C. Barash Michael R. Fannon TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5256 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Appl
Appl
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                                                                                              (without alignments)
5417.965 Million cell updates/sec
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                                                                                  6, 2004, 04:13:01; Search time 135 Seconds
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS COMB.seq:*
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Compugen Ltd.
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US-08-36-165A-179
US-08-714-918-61
US-09-265-315-61
US-09-265-315-61
US-09-263-715-61
US-09-528-709-61
US-09-528-709-61
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    GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Listing first 45 summaries
                                                         OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                             OLIGO_NUC
Gapop_60.0 , Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                   Issued Patents NA:*
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length: 2000000000
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Match Length DB
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Minimum DB Maximum DB

Database

Result

0 0 0 0 0 0 0

Word size

Searched:

Sequence:

Title:

Run on:

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CATGTTATGAATGGTGATAAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA 1046
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MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
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                                                                                                                                                                                                                 APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFRENCE/DOCKET NUMBER: PB248P1
                                                                                                                          APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1314; I
Pred. No. 0;
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SEQUENCE DESCRIPTION: SEQ ID NO: 392:
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TELEPHONE: (240) 314-1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.7%; Sco.
100.0%; Pre
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LENGTH: 2424 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 392:
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STRANDEDNESS: double
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180 806 240

866 300 926 360

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961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
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                                                                                    CITY: King of Prussia CITY: King of Prussia STATE: PA

COUNTY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: DASTEM: DOS
SOFTWARE: FAST-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFCATION NUMBER: 60/027,032
FILING DATE: ALSEP-1996
ATTORNEY AGENT INFORMATION:
NAME: Gimmi, EGWART R
                                                 Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAACCACACATTTCTCTAGAACACA 1046
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PS
TELECOMMUNICATION INFORMATION:
                                               E: SmithKline Beec
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 619 base pairs
TYPE: nucleic acid
FYRANDEDNESS: single
TOPOLOGY: linear
MOLECTUE TYPE: Genomic DNA
US-08-936-165A-179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 610-270-4478
  534
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                           CORRESPONDENCE ADDRESS:
  NUMBER OF SEQUENCES:
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                                            ADDRESSEE:
                                                                       STREET:
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                                                                                                                                                                   099
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                                                                                                1167 GATATTAATGATGTTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT
                                                                                                                                                                                                                                                                                          TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAAAAATACTGGCGCA
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                                                                                                                                                                   ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT
                                                                                                                                                                                                                                                                 TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knowles, David
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
APPLICANT: Pratt, Ullie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
TITLE OF INVENTION: No. 6348582el Prokaryotic Polynucleotides,
TITLE OF INVENTION: Polypeptides and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-08-936-165A-179/c
; Sequence 179, Application US/08936165A
; Patent No. 6348882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
                                                                                                                                                                   601
                                                                                                                                                                                                                                                                 661
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CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Lyon & Lyon
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
    NUMBER OF SECUENCES: 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
US-09-265-315-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-265-315-61/c
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STREET: 63
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| Sequence 61, Application US/09265315
| Setent No. 6187541
| GENERAL INFORMATION: Bret
| APPLICANT: Beaton, Bret
| APPLICANT: Malouin, Francois
| APPLICANT: Malouin, Patrick K. APPLICANT: Schmid, Molly B. APPLICANT: Schmid, Molly B. |
| TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS |
| TITLE OF INVENTION: TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 888;
APPLICANT: Malouin, Francois
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Submid, Molly B.
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.8%; Score 90; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 8.6e-33;
Matches 90; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
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                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.

IIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compactible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,102
RILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATIONNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                       ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-08-714-918-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-265-315-61/c
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TELEX: 6'
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Fatent No. 6187541
GENERAL INFORMATION:
APPLICANT: Bencon, Bret
APPLICANT: Malouin, Francois
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Domgxu
ITILE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
ITILE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
ITILE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
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                                                                                                               COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
COMPUTER: IEM Compatible
COMPATE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIFICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: September 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REJERRENCE/DOCKET NUMBER: 32,327
TELECOMMUNICATION NUMBER: 32,327
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION 1995-0440
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
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507 Arradakcaarricaraariccicriarrir 478
     NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STRERT: 633 West Fifth Street
Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lee, ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
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; Sequence 61, Application US/09528709
; Patent No. 6630303;
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-09-266-417-61
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Sequence di, Application US/09266417

Patent No. 622858

GENERAL INFORMATION,
APPLICANT: Benton, Bret

APPLICANT: Malouin, Francois
APPLICANT: Markin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.8%; Score 90; DB 3; L. 100.0%; Pred. No. 8.6e-33; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1209 ATTAGAACAATTIGATAATGCTGTTATTTT 1238
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                                                                                                                     MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: MARCH 9, 1999
CLASSIFICATION: 435
FILING DATE: September 13, 1996
APPLICATION NUMBER: 06/1009,102
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/003,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 32,327
REFERENCE/POCKET NUMBER: 240/247
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ 13) 955-0440
TELECOMUNICATION SEQ 1D NO: 61:
                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100. Matches 90; Conservative
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
US-09-265-315-61
                                                   RY: U.S.A.
90071-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-266-417-61/c
                  CITY: LOS
STATE: CZ
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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567 ACAAGATTTAATTGALAAATTGAAGGTGCATCGTTAATTAATGAAGATTCTATTAATGT 508
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Query Match
6.8%; Score 90; DB 3; Length 888;
Best Local Similarity 100.0%; Pred. No. 8.6e-33;
Matches 90; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                            1209 ATTAGAACAATTTGATAATGCTGTTATTT 1238
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Search completed: June 6, 2004, 07:10:16
Job time : 136 secs
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Lee, Vining
Lee, Vinin, Francois
Malouin, Patrick K.
Schmid, Molly B.
Sun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: Word Perfect 5.1
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,709
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 ATTAGAACAATTTGATAATGCTGTTATTTT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.8%; Score 90; DB Best Local Similarity 100.0%; Pred. No. 8.6 Matches 90; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,745
                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REPERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/09527745
Patent No. 6638718
GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-527-745-61/c
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567 ACAAGATITAAITGATAAAITGAAGGIGCATCGTIAAITAATGAAGATICTATTAATGT 508
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.8%; Score 90; DB 4; Length 888;
100.0%; Pred. No. 8.6e-33;
Live 0; Mismatches 0; Indels
                                                 APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/09,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY, AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
TELEPRONE: (213) 489-1600
TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1209 ATTAGAACAATTTGATAATGCTGTTATTTT 1238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            507 ATTAGAACAATTTGATAATGCTGTTATTTT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE DESCRIPTION: SEQ ID NO: 61:
FILING DATE: 17-Mar-2000
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTER.STICS:
LENGTH: 888 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                       PRIOR APPLICATION DATA:
```

```
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
```

June Run on:

OM nucleic - nucleic search, using sw model

6, 2004, 04:34:41; Search time 315 Seconds (without alignments) 5591.218 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-712-713-1 1318 1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318

OLIGO_NUC Gapop_60.0 , Gapext 60.0

Scoring table:

2089662 seqs, 668146292 residues Searched:

20

Word size :

0 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Pending Patents NA New:*

1: /cgn2 6/ptcdata/2/pna/DST NEW COMB.seq:*

2: /cgn2 6/ptcdata/2/pna/USO6 NEW COMB.seq:*

3: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

4: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

5: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

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7: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

7: /cgn2 6/ptcdata/2/pna/USO8 NEW COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description

Query Score Match Length DB Result

No matches found

6, 2004, 08:36:08 Search completed: June Job time : 315 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

June

US-10-712-713-1 1318

Title: Perfect score:

1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318 Sequence:

OLIGO_NUC Gapop_60.0 , Gapext 60.0 Scoring table:

27513289 seqs, 14931090276 residues Searched:

20 Word size : Total number of hits satisfying chosen parameters:

0

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

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gb_est::*
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gb_est::*
em_estro:*
em_gsest::*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Score Match Length DB

Result

Description

No matches found

Search completed: June 6, 2004, 07:07:51 Job time: 3824 secs

BX415878 BX415878 BX437758 BX437758 BX437758 BX45575 BX45609 ENTEWS3TF BJ376728 BX415058 BU498120 PfEST0ab9 BJ31309 DAILO FE BX13987 BX415097 BX13987 BX415097 BX13987 BX415097 BX43979 BX439779 AL281758 BX437758 BX43979 BX437758 BX437758 BX437758 BX337758 BX437758 BX37756 BX437739 BX176523 BY38069 BH178274 011 F 07-AL615231 T7 end of AL615231 T7 end of BX37756 BX37756 BX376618 BX461824 BH204978 SM1-4319. AZ528468 ENTCM64TF AZ676218 ENTRGSETF

on:

Run

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2937 DNA linear GSS 01-MAY-20
LLMGtag738 MG1363 Random Sequence Tag Library Lactococcus lactis
subsp. cremoris genomic, genomic survey sequence.
BH771016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domaine de Vilvert, 78352 Jouy en Josas cedex, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactococcus lactis subsp. cremoris
Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 2937)
Bolotin,A., Ehrlich,S.D. and Sorokin,A.
Studies of genomes of dairy bacteria Lactococcus lactis
Sci. Aliments (2002) In press
Contact: Sorokin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 33 134 65 25 16
Fax: 33 134 65 25 16
Fax: 33 134 65 25 21
Bmail: sorokine@jouy.inra.fr
Bmail: sorokine@jouy.inra.fr
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 2907.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
            BX437758
CNS00EVL
AZ548467
BX456575
BX3546009
BJ376729
BX415058
BX415058
BX415987
AZ551048
BX139972
BX39739
CNS04AEE
BX437758
BJ374223
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DEFINITION
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KEYWORDS
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BH384961 AG-ND-161
BH400896 AG-ND-145
AL063921 Drosophil
                                                                                                         (without alignments)
10292.457 Million cell updates/sec
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                                                                                                                                                                     1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                           5, 2004, 23:40:14; Search time 3824 Seconds
                                                                                                                                                                                                                                                              55026578
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                      27513289 seqs, 14931090276 residues
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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BH384961
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CNS0039G
                                                                   - nucleic search, using sw model
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                                                                                                                                             Title:
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GSS 01-MAY-2002

No.

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Result

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845 TTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAATGAAA
                                                        334 reacagargriccicaccicricaccricriccaagaagaaaaaaccccrirracreaga
                                                                                                                    905 CTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTG
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/clone="AG-ND-161118"
/clone_lib="ND-TAM"
/note="Vector: pECBAC1; Site_1: HindIII"
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Mol. Genet. Genomics 268 (6), 720-728 (2003)
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/mol_type="genomic DNA"
/gtrain="PEST"
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Contact: Brendan J Loftus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BH384961.1 GI:17331103
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                                                                                                                                                       /sub_species="cremoris"
/db_xref="taxon:1359"
/clone lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site 1: Sma1; Library of
chromosomal fragments of L.Tactis strain MG1363 was
prepared by partial AluI digestion or by sonication."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      Score 373.6; DB 28; Length 2937;
Pred. No. 4e-68;
0; Mismatches 454; Indels 5;
                                                                        'organiem="Lactococcus lactis subep. cremoris"
                                                                                                 /mol_type="genomic DNA"
/strain="MG1363"
               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         28.3%;
59.4%;
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Best Local Similarity 59.4%
Matches 671; Conservative
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
F.H. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
to minimize the inclusion of DNA from microorganisms that inhabit
the gut. The DNA is derived from mixed sexes of larvae. The BAC
library was constructed at Texas A&M Universty BAC Center
University, College Station, Texas 77843-2123, USA using a HindIII
                                                                                  1024
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Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J., Ren, C., Huff, B.R., Carlile, J.L., Black, K., Zhang, H.-B., Gardher, M.J. and Collins, F.H.
Construction of a BAC library and generation of BAC end sequence-tagged connectors for genome sequencing of the African
                                                                              965 CTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAAC
                                                                                                                                                                                                                                                                                                                          154 crcaracaritraccacacarrecririrecreaticactrirecreatical
                                                                                                                                                                 214 CAACATTGGATGCGGCTCGTCAAAAATATCCTGACCGTGAAATCGTTGCGGTATTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Eukaryota; Metazca; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                        1085 CAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACT 1134
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Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                  'note="Vector: pECBAC1; Site_1: HindIII"
                                                                                                                                                                                                                                                                                                                                                             6.5%; Score 85.8; DB 28;
ilarity 52.4%; Pred. No. 8.6e-08;
Conservative 0; Mismatches 172;
                                                                                                                  Location/Qualifiers
1.584
1.084
.organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="AG-ND-145A13"
/clone_lib="ND-TAM"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bjloftus@tigr.org
This clone is from an A. gambiae BAC library (ND-TAM) provided by
This clone is from an A. gambiae BAC library essenth
Th. Collins and sequenced by The Institute for Genomic Research
(TIGR). The BAC library was generated from A. gambiae PEST strain
DNA. All DNA was extracted from newly hatched first instar larvae
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Hong, Y.S., Hogan, J.R., Wang, X., Sarkar, A., Sim, C., Loftus, B.J.,

Hong, Y.S., Hogan, J.R., Carlile, J.L., Black, K., Zhang, H.-B.,

Gardner, M.J. and Collins, F.H.

Construction of a BAC library and generation of BAC end

sequence-tagged connectors for genome sequencing of the African
malaria mosquito Anopheles gambiae

Mol. Genet. Genomics 268 (6), 720-728 (2003)
                                                                                                                             624 GGAGCAAGCTATGAAGATCTTAAAAAAAAGGAATTAAATCTTTCAAAGGGATTAAAAGAAG
                                                                                                                                                                                                                                                                                                                                               1011 TGCAGTATTTCAACCACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGA
                                                                                     834 GAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCG
                                                                                                                                                                       894 TTTCAATGAAACTACAATTGCAAAT---CAAGTTATTGTAGATGATTATGCACACCATCC
                                                                                                                                                                                                                  504 AACTGAGCTAAATGCTGTAATTGGTTCCATAAAAACCTTTTATCCCGATAAAAAGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 AAGTTTGAGTAAAGGAGAAGAGTTGATTTTATTAGATATATCCAGCTCGTGAATTGCC
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
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    Length 728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                          Indels
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The Institute for Genomic Research
Thy Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
Score 90; DB 28; L. Pred. No. 1.1e-08; 0; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1251 AGGTGATATTCAAAATTACAAAATGCATA 1280
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Contact: Brendan J Loftus
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  Query Match
Best Local Similarity 51.6%;
Matches 232; Conservative
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BH400896/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಗ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1220 TTGATAATGCTGTTATTTTATGGGTGCAGGTGATATTCAAAAATTACAAAATGCAT 1279
to minimize the inclusion of DNA from microorganisms that inhabit the DNA is derived from mixed sexes of larvae. The BAC library was constructed at Texas A&M Universty BAC Center University, College Station, Texas 77843-2123, USA using a HindIII partial digest.
Seq primer: M13 For Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 920 AAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGAAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 AAATATATATAGATGACTATGCCCATCACCCAACTGAGCTAAATGCTGTAATTGGTTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1100 TATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 rraaaaaaaaarrrgararrcccrracagrogagcaggaararagaracrtsr
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Drosophila melanogaster
Bukaryot; Mercazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EST 15-MAY-2003

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/note="Vector: pcMVSBORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pcMVSBORT 6 vector. Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       729 WAYAAGAAWTATTAATACATANATATATATAWDCATAAAATATWAWTWTAWTAAATA 788
                                                                                                                  BX415878 15-MAY-2003
BX415878 Homo sapiens THYMUS Homo sapiens cDNA clone CS0CAP008Y104
                                                                                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.

(Dases 1 to 1200)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Linvitrogen. Conteact : Feng Liang Email : Filangabilfetech.com URL
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPO08BE02QP1.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              609 IWITWITITATITITATATWIWITITIAALAATWAATATAAAATATITAAWIWRAWWAAWI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                477 AAGTTATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         597 TATTATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       549 TITITITAAATATITITAAAAAAAAAAATWAMTITIWITITITIWIMAAAWWITITIAIWITITIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     657 TIATTATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 GGGKKKGGGGGGGDWWWWTTTTWTTTWHMAAADCTTAWTWHTWHCCAISTTISCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         417 GGGATTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 5.9%; Score 77.8; DB 13; Length 1200; Best Local Similarity 33.9%; Pred. No. 3.9e-06; Matches 282; Conservative 115; Mismatches 430; Indels 4;
440 TITWIWITWWAATTAITITTTTTWTAAAAAAWWWWWIWIATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/mol_type="mRNA"
/db xref="taxon:9606"
/db xref="taxon:9606"
/tissue type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
                                                                                                                                                             5-PRIME, mRNA sequence.
BX415878
                                                                                                                                                                                                              BX415878.1 GI:30765550
                                                                                                                                                                                                                                                          sapiens (human)
                                                                                                                                                                                                                                                                                    Homo sapiens
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ORGANISM
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BX415878
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       셤
                     melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        958 ATTAGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTA 1017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1018 TITCAACCACACACTITCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTA 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1078 AGTAAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGC 1137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |: | :: :: : | : :: : | | :: : : : | DGGAGDKODGKGKGTWGDATWAWAAADDWWWWGWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGATAAACGTCGTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            738 TAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRRRRDRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    678 TWDRTDAWWADAAWWTTTDTDTDDWDKRDRRRKGARRRRTTARAAWDWWTWKAWDWAKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538 AAAGATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          598 ATTATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTAT
         The BDGP is constructing a physical map of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db Xref="taxon:7227"
/clone="BACR0810"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.2%; Score 81.8; DB 29;
.larity 17.7%; Pred. No. 5.7e-07;
Conservative 300; Mismatches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="RPCI-98"
/note="end : TET3"
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es 125; Conserv
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: sequref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invircogen. Contact : Feng Liang Email : fliang@lifetech.com URL
http://fulllength.invircogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP008CA01QP1.
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/close lib="HGMO sapiens THYMUS"
/close lib="HGMO sapiens THYMUS"
/note="Wector: pCHVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned in
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>CAATGAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGA</u>
                                                                                                                                   AAGTAAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGG
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                                                TTTWAWAATWACAAAATWAAAAAAWTTTAAAAAWTTWTAAATTWAAAAAWAATTTTA
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Li,W.B. Gruber,C., Jessee,J. and Polayes,D.
Li,W.B. Gruber,C., Jessee,J. and Liayes,D.
Unpublished (2001)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOCAP008YB01"
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5-PRIME, mRNA sequence.
BX437758
BX437758.1 GI:30773605
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Length IndelB

Query Match 5.9%; Score 77.8; DB 13; Best Local Similarity 31.6%; Pred. No. 3.9e-06; Matches 272; Conservative 169; Mismatches 404;

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                                               505 ACAAATATTGATTTCGATCATCCTGATTATTTTAAAGATATTAATGATGTTTTTTGATGCA
                                                           GATWITTTTTTTTWAARGDWKWTWTWTTTTTTTTTTT------TTTWTTGTTTW
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                     TIGGGGGDWITIWWWIWIAARRDKITITITITIWAAAAARATAKRGGRGGADAWITAWWI
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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/db xrefe="taxon:5759"
/db xrefe="taxon:5759"
/clone lib="Entamoeba histolytica Sheared DNA"
/clone lib="Textamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: BET I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond, LiS.
C.G., and Diamond, LiS. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                         GSS 14-NOV-2000
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ENTEK30TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota, Entamoebidae, Entamoeba.
I (bases 1 to 908)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
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AZ548467
AZ548467.1 GI:11172102
                                             991 ATTWWIAWTAWATATTTATTAA 1015
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/strain="HM1:IMSS"
1290 ATTAGGCATGAAAATGCGTTTTAA 1314
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High quality sequence stop: 828.
Location/Qualifiers
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Seq primer: M13-Reverse
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    ਨੋ
                                                                                                                                                                                                                                                                         Web: www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and mannoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT.98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACPRC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---TGATTATGCACACCATCCAAGAGAAATTAGTGCTACAATTGAAACAGCACGAAAGAA 989
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Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliangeliferech.com U
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP002DB02QP1.
Location/Qualifiers
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Mammalia; Eutheria, Primates; Catarrhini, Hor
1 (bases 1 to 1099)
Lil,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
5-PRIME, mRNA sequence.
BX456575
BX456575.1 GI:31034783
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/clone="CSOCARPO02YD04"
/tissue type="THYMUS"
/clone_lib="Howers prient THYMUS"
/clone_lib="Howers prient THYMUS"
/note="Vector: pcWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned it the Not I and EcoRV sites of the pcWVSPORT 6 vector. Library was not normalized."
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Entamoeba histolytica
Enkaryota, Entamoebidae, Entamoeba.
1 (bases 1 to 849)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
                                                                                                                                                                                                                                                                                                                                                              1098 AAKAABAATKAKABAAWKAKAKKDAWRAADDDKATAAWKKRATKADAARADAATKWKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 AATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGA--CAGATTATTGATCAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TKKRGTKKDKRDAKKKGGARAKKKGRAWKTKKKGAAARRAAWAARWAAAAAAAATATK
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                                                                                                                                                                                                                                                                                                                                                                                                                          303 TACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICIACAACAGGITIATIAICACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGATTTAAAGATTCGCATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTAC
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                                                                                                                                                                                                                                                                                 2;
                                                                                                                                                                                                                                    Query Match 5.4%; Score 71.8; DB 13; Length 1099; Best Local Similarity 26.6%; Pred. No. 7.2e-05; Matches 157; Conservative 169; Mismatches 263; Indels 2;
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1000 AAAGAAGTIGTIGCAG
                                  91 GATGAAGATGATGAAG
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Best Local Similarity 46.8
Matches 253; Conservative
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/clone lib="Entemocha histolytica Sheared DNA"
/note="Wector: pHOS1; Site 1: Bet I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of B. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entemocha histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                   Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 TTTGAATTAGAAGATGAAGAAGATGAAGATGATGATGAAGACGAAGAAGACGAAGATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATCATCCTGATTATTTTAAAGATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCA
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Pred. No. 0.00014;
0; Mismatches 266; Indels 0
                                                                                                                                                                                                                                                                                                                   'organism="Entamoeba histolytica"
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                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="HM1:IMSS"
                                                                                                                                                                                                                                        High quality sequence start: 26
High quality sequence stop: 796.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         'db_xref="taxon:5759"
   HM1:IMSS sheared DNA library
                   Unpublished (2000)
Contact: Brendan J Loftus
                                                                                                                                                                                                      Seq primer: M13-Forward
Class: shotgun
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ilarity 46.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           452 TAATAAGAAATTTAATAAGAAATTAGATATTACAGGTAGTGATGAAGAATATGATGATGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 GACAAATATTGATTTCGATCATCCTGATTATTTAAAGATATTAATGATGTTTTTTGATGC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 TIATCAAGAAGAAGATTIGAAGATGAAAACCIGAAAATTCAAATTATAATAAAAATT 273
BJ376728
BJ376728 Dictyostelium discoideum cDNA library, CF Dictyostelium discoideum cDNA sequence.
                                                                                                                                                                          Dictyostelium discoideum
Dictyostelium discoideum
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
1 (Dases 1 to 754)
Urushihara, H., Tanaka, Y., Kohara, Y. and Shin-i, T.
Pull length cDNA of Dictyostelium discoideum at the culmination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 572 TGAAGAAGAGAAAAAGAAATCAAAAGAAATGGATGAAGAATTGGATAAAATTGAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIGAGGCATGIGAATATAGACGICACTTTTTAAGTTATAAACCTGATTACGCAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACGTAAAATTGAAGCAGATGTTCCAATTTATTATTATGGATTTAAAAGATTCGGATGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev stage="Culmination stage"
/clone_lib="Dictyostelium discoideum cDNA library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ښ</u>
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                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
Tal: Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6856
Fax: 1-559-81-6856
Fax: L-559-81-6856
Fax: L-559-81-6856
Fax: L-559-81-6856
Fax: L-559-81-6856
Fax: L-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Dictyostelium discoideum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 69.6; DB 12;
Pred. No. 0.00021;
0; Mismatches 285;
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/clone="ddc29013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="AX4"
                                                                                            BJ376728
BJ376728.1 GI:19286111
EST.
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/mol type="marka"
// db xref="taxon:36329"
/lab host="blue"
/lab host="blue"
/lab host="blue"
/lab host="blue"
/clone lib="plasmodium falciparum ib7 asexual cDNA"
/clone lib="plasmodium falciparum ib7 asexual cDNA"
/clone lib="plasmodium falciparum ib7 asexual cDNA"
/clone library was constructed by Debopam Chakrabarti.
Xhof; Library was constructed by Debopam Chakrabarti.
Total RNA samples were isolated from mixed stage
saponin(0.1%)-lysed P. falciparum ib7 infected
erythrocytes by the acidic guanidinlum-phenol chloroform
method. The poly A+ RNA was isolated by the polyAT-Tract
mRNA isolation system (Fromega, WI) using streptavidin
Magnesphere particles. Directional cDNA libraries were
constructed by oligo d(T) priming of poly(A) + RNA (5mg)
into BockI and XhoI sites of I zapiI vector using the Zap
cDNA synthesis kit (Stragene, CA). The average size of the
cDNA inserts in the library was between 1.0 and 1.5kb.
Clones were mass excised using the ExAssist helper phage
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Fig. 11-SEP-2002

FESToab93a09.yl Plasmodium falciparum 3D7 asexual cDNA Plasmodium falciparum 3D7 cDNA Fismodium falciparum 3D7 cDNA Fismilar to TR:096253 096253 HYPOTHETICAL 220.3 KD PROTEIN. ;, mRNA sequence.
                                                                                                                                                                                                                                              ATTTTTGGATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAA 1167
                                                                                                                                                                                                                                                                                                                                                                                                                1168 ATTGAAGGTGCATCGTTAATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAAT 1227
                                                                                                                                                                                                                                                                                                                               477
656 AAAAAMAYATHTATAWAAAATATWTWAAWAAWAAWAAAAAAAAAACATWTTWCAAAAWTTWT 597
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 594)

1 (bases 1 to 594)

1 (bases 1 to 594)

Marra,M., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,B., Bennett,J., Jentes,E., Ronko,I., Tsagareishvili,R., Belaygorod,L., Franklin,C., Carr,L., Grow,A., Maguire,L., Richey,J., Wadkins,J., Kennedy,S., Levinso,D., Washu Plasmodium EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: estowatson.wustl.edu
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Library was constructed by Debopam Chakrabarti DNA sequencing by:
Mashington University Genome Sequencing Center For information on obtaining a clone please contact: L. David Sibley
(sibley@borcim.wustl.edu), Washington University
Seq primer: -40UP from Gibco
High quality sequence stop: 422.
Location/Qualifiers
                                                                                 GCATTITIAAATGAATTITGCAGAAAGTITAAGTAAAGCAGATCGTGTATTCTTATGTGAA
                                                                                                                                                             536 TTTTTTTTTTATATAWMMMHWAATWTTTWTTTWAATTWTWATAAAAWTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1228 GCTGTTATTTTATTTATGGGTGCAGGTGATATTCAAAAATTACAAAATGCATAT 1281
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium falciparum 3D7"
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Contact: L. David Sibley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BU498120.1 GI:22794314
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/tissue_type="FETAL BRAIN"
/dev stage="fetal"
/clone_lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSPORT 6
vector. Library was not normalized."

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Gaps

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670 302 362 790 422 850 482 910 542

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AAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGCTTTTG 730
                                                                             (Stratagene), the phagemids were preciptated with PEG 8000 and extracted with phenol/chloroform. Phagemid DNA was electroporated into DH10B cells."
                                                                                                                                                                                                                                         491 ATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAAGATATTAAATG
                                                                                                                                                                                                                                                                                                          ATGITITIGATGCATICCAAGAAATGGCACATAATGTTAAAAAAAGGTATTATTGCTTGGG
                                                                                                                                                                                                                                                                                                                                          791 CAGTITITAAAIGCATTAGCIGIAAIIGCGATIAGTIAITITAGAGAAGCIAGAIGTIACAA
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Pred. No. 0.00042;
0; Mismatches 238; Indels 0
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                                                                                                                                                                      Query Match
Best Local Similarity 47.0%;
Matches 211; Conservative (
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AL536104 10mc sapiens FETAL BRAIN Homo sapiens cDNA clone CSODF022YC18 5-PRIME, mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
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Contact: Genoscope

Control National de Sequencage
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
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Wall-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:12799597.
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AUTHORS
TITLE
JOURNAL
COMMENT
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AUTHORS

organiem="Homo eapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DF022YC18"

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1013
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(Ypriniformes, Cyprinidae, Danio.

1 (Dases 1 to 844)

Humphray, S. J., Huckle, E. and Durham, J. L.
                                                                                                                                                                                                                            TTGGTGGTGTTAAACGTCGTTTCAATGAAACTACAATTGCAAATCAAGTTATTGTAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                458 AATATAGACGTCACTTTTTAAGTTATAAACCTGATTACGCAATTATGACAAATATGATT
                                                                                                                                                                                                                                                             ATCACTTCCTGTCTCCACAATATGGTGACCATACAGTTTTAAATGCATTAGCTGTA---A
                                                                                                                                                                                                                                                                                                                                       894 TITTTAITTATAAWTITWTAWAWNAITWTWWWAATWAITAGWIAWWAWWAATATATA
                                                                                                                                                                                                                                                                                                                                                                TTGCGATTAGTTATTTAGAGGTAGATGTTACAAATATTAAAGAAGCATTAGAAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    995 CACATAAAGAAGTTGTTGCAGTATTTCAACCACACACTTTCTCTAGAACACAGGCATTTT
                                                                             AAGCAGATGTTCCAATTTATTATTATGGATTTAAAGATTCGGATGACATTTATGCTCAAA
                                                                                                       518 TCGATCATCCTGATTATTTAAAGATATTAATGATGTTTTTGATGCATTCCAAGAAATGG
                                                                                                                                                         CACATAATGTTAAAAAAGGTATTATTGCTTGGGGGTGATGATGAACATCTACGTAAAATTG
                              Gaps
                             ω
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/ Match 5.1%; Score 67.8; DB 9; Length 1201; Local Similarity 32.1%; Pred. No. 0.00049; nes 195; Conservative 112; Mismatches 298; Indels 3
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1194 TAWADRWW 1201
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Best Local Si
Matches 195;
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TITLE Direct Submission
JOURNAL Submitted (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinton, Cambridgeahire, CB10 15A, UK. E-mail enquiries:
humquery@sanger.ac.uk'upublished
COMMENT This sequence was generated from the T7 end of BAC 9987. 9987 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
Keygene. Further details:
http://www.sanger.ac.uk/Projects/D_rerio/.
```

Query Match
5.1%; Score 67.2; DB 29; Length 844;
Best Local Similarity 50.0%; Pred. No. 0.00067;
Matches 168; Conservative 0; Mismatches 168; Indels 0; Gaps
Oy 426 TGAAAGTGATTATTTGAGGCATGTGAATATAGACGTCACTTTTTAAGTTAAAA 4

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 666 ATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGC 725

667 TAATAATAATAATAATAATGATGATAATAATAATAA 702

726 TITIGAIGIGIAIGIGGAIGGIGAGITITAIGAICA 761

Search completed: June 6, 2004, 02:44:40 Job time : 3829 secs

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Protein

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Abp56614 S. pneumo
Adc94287 E. pneumo
Adc97287 E. aeciu
Abu24704 Protein e
Abu23758 Protein e
Abu15770 Protein e
Abu15770 Protein e
Abu353736 Acinetoba
Abu33503 Protein e
Aay74417 Naisseria
Abu38150 Protein e
Ay74417 Naisseria
Abu3957 Protein e
Ay74418 Naisseria
Abu3957 Protein e
Ay74418 Naisseria

June

Run on:

OM protein

score:

Perfect

Title:

Sequence:

Scoring table:

Total number Minimum DB &

Maximum

Database

Searched:

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isolated nucleic acid for use in diagnosing Staphylococcus infections in vaccines for eliciting immune responses to the infections.
                                                                                                                                                                                                                                                                                                                                                  UDP-N-acetylmuramate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents S. aureus Murc (UDP-N-acetylmuramate:L-alanine ligase). The polynucleotides of the invention are used to detect Staphylococcus nucleic acids in a biological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention
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ABU37200
AAY74417
ABP80545
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ABU25700
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AAY74419
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ABU35149
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ADC45197
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ABU24704
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Staphylococcus aureus.
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N-PSDB; AAS00189
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Query Match

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1298.5 1180

1163.5 1139 1132.5 1119 1119 1119

us-10-712-713-2.rag

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from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genue and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, joint infection, meonatal conjunctivitis, osteomyelitis, skin infection, escaled skin syndrome (also known as toxic epidermal necrosis, Ritter's disease and izyell's disease), toxic shock syndrome and endocarditis. The polymucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods
used to detect anti-Staphylococcus antibodies in a biological sample
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Sequence 437 AA;

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100.0%; Score 2275; DB 4; 100.0%; Pred. No. 9.7e-193;
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The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention

Sequence 444 AA;

New Staphylococcus aureus protein, useful as a vaccine for treating or preventing Staphylococcal infection, specifically an infection caused by S. aureus, e.g. sepsis.

Ξ

Scarselli

Masignani V, Mora M, 2003-120786/11.

N-PSDB; ACF72770

(CHIR-) CHIRON SPA

27-MAR-2001; 2001GB-00007661

Claim 1; SEQ ID NO 900; 49pp; English.

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8 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE
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                                      Gaps
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                                      Indels
Query Match
100.0%; Score 2275; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.9e-193;
Matches 437; Conservative 0; Mismatches 0;
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Staphylococcus aureus protein #450.

(first entry)

enzymatic assay; antibiotic target

Staphylococcus aureus

Antibacterial; vaccine;

27-MAR-2002; 2002WO-IB002637.

28-NOV-2002

ABM71210 standard; protein; 444 AA.

KESULT 2 ABM71210

240

247 300 307 360

367 420 427

Mon

27-MAR-2003

immunological response; vaccination; shrface disinfectant; personal hygiene application; food preservative; enzyme; MurC; UDP-N-acetylmuramate-alanine ligase. microbial; antimicrobial; membrane biodynthesis; pathogenic; Staphylococcus aureus MurC protein (SeqID 30)

Staphylococcus aureus.

WO2003025007-A2.

20-SEP-2002; 2002WO-CA001428

2001US-0324152P. 2001US-0324692P. 30-OCT-2001; 2001US-0340924P. 27-NOV-2001; 2001US-0333666P. 2001US-0350973P. 2001US-0341732P. 2001US-0323992P 2001US-0339924P 2001US-0341776P 21-SEP-2001; 21-SEP-2001; 25-SEP-2001; 26-OCT-2001; 29-OCT-2001; 18-DEC-2001; 18-DEC-2001;

2001US-0341949P (AFFI-) AFFINIUM PHARM INC. 19-DEC-2001;

Vedadi M, Alam MZ, Awrey D, Beattie B; Kanagarajah D, Nethery K, Ng I, Mansoury K; Viola C, Wrezel O; Dharamsi A, Houston S, Pinder B, V Edwards A, Domagala M, Mcdonald M,

XX II II

2003-468119/44. N-PSDB; ADD15464. Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Claim 20; SEQ ID NO 30; 325pp; English.

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli) that provide novel antimorobial targets. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the characteribes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also functional the side of the control of these proteins that facilitate function describes not the structural and functional developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polypeptide sequence is the MurC protein encoded by experimentally predicted DNA from S. aureus UDP-N-acetylmuramate-alanine ligase of the invention. information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for

Sequence 444 AA;

ö Gaps <u>,</u> Length 444; Indels Score 2275; DB 7; Pred. No. 9.9e-193; ô 0; Mismatches 100.0%; Query Match
Best Local Similarity 100.
Matches 437; Conservative

9 67 MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120

300 180 240 127 187 247 307 360 367 420 427 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLBKLDVTNIKEALETFGGVKRRFN HVMNGDKKTSFLIGDGTGMGLPESDYPAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK DINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRFN **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVRQPHTFSRTQAFLNEFAESLS ETTIANOVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTOAFLNEFAESLS** 368 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINRDSINVLEQFDNAVILFMGAGDI QKLQNAYLDKLGMKNAF 437 OKLONAYLDKLGMKNAF 444 248 308 68 121 128 181 188 241 301 361 421 428 ò 셤 ò 셤 8 셤 à 요 8 d Š

RESULT 4 ADD15463

ADD15463 standard; protein; 444 AA.

ADD15463;

(first entry) 15-JAN-2004 Staphylococcus aureus MurC protein (SeqID 28).

microbial; antimicrobial; membrane biosynthesis; pathogenic; immunological response; vaccination; surface disinfectant; personal hygiene application; food preservative; enzyme; MurC; UDP-N-acetylmuramate alanine ligase.

Staphylococcus aureus

WO2003025007-A2.

20-SEP-2002; 2002WO-CA001428 27-MAR-2003

2001US-0324152P 2001US-0350973P. 2001US-0340924P. 2001US-0333666P, 2001US-0341732P, 2001US-0323992P 2001US-0339924P 29-OCT-2001; 30-OCT-2001; 27-NOV-2001; 21-SEP-2001; 25-SEP-2001; 26-OCT-2001; 21-SEP-2001; 18-DEC-2001;

2001US-0341776P 2001US-0341949P

19-DEC-2001;

(AFFI-) AFFINIUM PHARM INC.



Beattie B; I, Mansoury K; Alam MZ, Awrey D, 1 D, Nethery K, Ng Kanagarajah D, Viola C, Wrezel Vedadi M, Dharamei A, Houston S, Pinder B, V Domagala M, Mcdonald M, Edwards A,

2003-468119/44.

N-PSDB; ADD15462. THE CONTRACTOR OF THE STATE OF

Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in

membrane biosynthesis, useful as targets for pathogenic bacteria.

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus),

Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)

that provide novel antimicrobial targets. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also fusion proteins. These proteins provide structural and functional information to aid the discovery of therapeutic molecules to treat discorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for an antigen for vaccination purposes. developing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating food products to eliminate potential pathogens. This polypeptide sequence is the MurC protein encoded by DNA predicted from the genomic sequence of S. aureus UDP-N-acetylmuramate-alanine ligase of the invention. Claim 20; SEQ ID NO 28; 325pp; English

Sequence 444 AA;

ö Gaps .; 0 DB 7; Length 444; Indels Query Match 100.0%; Score 2275; DB 7; Best Local Similarity 100.0%; Pred. No. 9.9e-193; Matches 437; Conservative 0; Mismatches 0;

120 127 67 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE WTHYHEVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS œ 61

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188 DINDVEDAFQEMAHNVKKGIIAWGDDEHLRKIEADVEIYYYGFKDSDDIYAQNIQITDKG DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 181

TAFDVYVDGEFYDHFLSPQYGDHTVINALAVIAISYLEKLDVTNIKEALETFGGVKRRFN

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247

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360 367 420

248 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 307 **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFINEFAESLS** 301

KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 368 361

308

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ABU15856 ID ABU15856 standard; protein; 437 AA. RESULT 5

ABU15856;

(first entry)

19-JUN-2003

XXXXXXXX

Protein encoded by Prokaryotic essential gene #1383.

design Antisense; prokaryotic essential gene; cell proliferation; drug

Staphylococcus aureus.

WO200277183-A2

03-OCT-2002

21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107

(ELIT-) ELITRA PHARM INC.

06-MAR-2002; 2002US-0362699P

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD, 'n Wang Wall

WPI; 2003-029926/02. N-PSDB; ACA19726.

screening New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 43780; 1766pp; English.

the nucleic acid inhibits proliferation of a cell. Also included are:

the folls antisense sequences given in the specification where expression

of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid

encoding a polypeptide whose expression is inhibited by the antisense

concleic acid; (2) a host cell containing the vector; (3) an isolated

polypeptide or its fragment whose expression is inhibited by the

conjugate acid; (4) an antibody capable of specifically binding

the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

confounds activity of a gene in an operon required for

proliferation; (7) identifying a compound that influences the activity of

the gene product or that has an activity against a biological pathway

crequired for proliferation; or that inhibits cellular proliferation; (8)

identifying a gene required for cellular proliferation of the biological

corpounds acityity; (11) aculture comprising strains in which the gene

compounds acityity; (11) aculture comprising strains in which the gene

compounds acityity; (11) aculture comprising strains in which the each of the strains is present in a culture or collection of

compounds; or (13) identifying the target of a compound that inhibits the

conjounts; or (13) identifying the target of a compound that inhibits the

creativity; of the strains is present in a culture or collection of

conjounts; or (13) identifying the target of a compound that inhibits or

creativity and organism. The antisense muleic acids are useful for

conditieration of an organism. The antisense muleic acids are useful for

for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at invention relates to an isolated nucleic acid comprising any one of ftp.wipo.int/pub/published_pct_sequences

Sequence 437 AA;

Gaps ö Length 437; Indels DB 6; .2e-192 Pred. No. 1.26 1; Mismatches Score 2274; 100.04; 99.88; Conservative Best Local Similarity Matches 436; Query Match

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9 1 MIHYHFVGIKGSGMSSIAQIMHDIGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 1 MIHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120

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                                           HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180
                                                                       180
HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK
                                                                                                                         181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                                                     TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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                                                                                                 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                          TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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AAU33801 standard; protein; 437 AAU3380 RESULT

AAU33801;

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(first entry)

14-FEB-2002

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Staphylococcus aureus cellular proliferation protein #77. Antisense; prokaryotic cellular proliferation protein antibacterial; drug design.

; antibiotic;

Staphylococcus aureus WO200170955-A2

21-MAR-2001; 2001WO-US009180

2000US-0191078P.

21-MAR-2000;

23-MAY-2000; 2000US-0206848P. 26-MAY-2000; 2000US-0207727P. 23-OCT-2000; 2000US-0242578P. 27-NOV-2000; 2000US-0253625P. 22-DEC-2000; 2000US-0257931P. 16-FEB-2001; 2001US-0269308P.

(ELIT-) ELITRA PHARM INC

Carr GJ; Trawick JD, Wall D, Zyskind JW, Ohlsen KL, Xu HH; Haselbeck R, Yamamoto RT,

WPI; 2001-611495/70. N-PSDB; AAS51660.

ŏ New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.

prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design

Antisense;

Staphylococcus aureus.

WO200170955-A2

27-SEP-2001

Example 3; SEQ ID NO 5297; 511pp; English.

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes

development. The antisence nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antishodies capable of binding to the expressed proteins, and to obtain antishodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in eflectronic format directly from WIPO at ö themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococous aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic 120 120 180 240 360 360 180 240 300 420 420 TAFDVYVDGBFYDHFLSPQYGDHTVLNALAVIAISYLBKLDVTNIKEALETFGGVKRRFN 300 9 9 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFGANNIKE DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKL,DVTNIKEALETFGGVKRRFN **ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVPQPHTFSRTQAFLNEFAESLS ETTIANQVIVDDYAHHPREISATIETARKKYPHKBVVAVFQPHTFSRTQAFLNEFAESLS** DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG KADRVFLCEI FGSIRENTGALTIQDLIDKI EGASLINBDSINVLEQFDNAVILFMGAGDI Gарв .; 0 Length 437; Staphylococcus aureus cellular proliferation protein #870. Indele Score 2267; DB 4; I Pred. No. 5e-192; 1; Mismatches 1; Æ AAU36700 standard; protein; 444 437 OKLONAYLDKLGMKNAF 437 99.64; QXC,QNAYLDKC,GMXNAF (first entry) Best Local Similarity 99.5 Matches 435; Conservative Sequence 437 AA; 14-FEB-2002 241 19 61 AAU36700; Query Match Best Local S 121 241 301 361 361 421 181 301 421 AAU36700 856666666666666666888 ਨੇ 셤 à ద à å Š a ठ g ð 셤 8 셤 ð 셤

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes theorem to their use in the discovery of novel antibiotics, the essential genes consisted in the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aurens, Salmonalla typhi, Klebbiela pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins con the compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present saquence represents an essential prokaryotic colorganisms. The present saquence represents an essential prokaryotic colorganisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the proposation of the proposa
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                                                                                                                                                                                                                                                                                                                      Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 12293; 511pp; English.
                                                                                                                                                                                                                                                                                                                   Zyskind JW,
                                                                                             2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
                                                                                                                                                                     2000US-0253625P.
2000US-0257931P.
                       21-MAR-2001; 2001WO-US009180.
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Matches 435; Conservative
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                                                                                                                                                                                                                                                                                                                      Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-611495/70.
N-PSDB; AASS4559.
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                                                                                                                                                                  27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
                                                                        21-MAR-2000;
23-MAY-2000;
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23-OCT-2000;
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Yamamoto RT,
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The present sequence represents a UDP-N-acetylmuramate:L-alanine ligase

(Murc polypeptide) encoded by the S. aureus Murc gene. Host cells

containing an expression system comprising the Murc gene can be used for

the recombinant production of the polypeptide. Agonists or the Murc

copyreptide are used to treat conditions requiring increased activity or

expression of the polypeptide. Antagonists, inhibitory nucleic acid or

competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting the polypeptide e.g.

Competitive polypeptide are useful for inhibiting they are also useful against

Competitial agents are useful to treat in-dwelling devices for

infection prevention or generally as wound treatments to prevent adhesion

of bacteria to matrix proteins. The Murc polypeptide is also useful for

diagnosing or prognosing a (susceptibility to) disease, for raising

contibodies, to identify modulators or specific receptors; in rational

drug design and as an immunogen for vaccines. The Murc gene sequences are

contibodies and in antisense/ribozyme therapeutics; to detect mutant Murc gene;

contibodies are contibodies and supping; to determine bacterial serotype; and for genetic
New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial
                                                                                                                                                                                                                                                                                                                                                                Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation.
                                                                                                                                                                                                                                                                                                                             UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide).
                                                                                                                                                                                                                AAW87771 standard; protein; 437 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 4; 39pp; English.
                                                                                   437
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                                                                                   OKLONAYLDKLGMKNAF
                                                                                                                    428 OKLONAYLDKLGMKNAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallis NG, Burnham MKR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-062655/06.
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1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE 60

98.4%; Score 2238; DB 2; Length 437; 98.2%; Pred. No. 1.8e-189; ive 3; Mismatches 5; Indels 0

Matches 429; Conservative

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Query Match Best Local Similarity

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                                                                                                                                                                                                                           ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS 360
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                                                       HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   open reading frame; ORF; bacterial infection;
               DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
                                                                       HVWNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK
                                                                                                                                                                   TAPDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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                                                                                                                                                                                                                                                                                               KADRVFLCEIFGSIRENSGALTIODLIDXIGGASFINEDLINVLEOFDNAVVLFMGAGDI
                                                                                                            DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                               DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                                                                                                                   ETTIANQVIVDDYAHHPREISATIDTARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLC
 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 5133; 267pp; English.
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gene therapy
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antibacterial;
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08-NOV-1997;
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particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycl or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug design.
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                                                                                                                                                                       1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE
                                                                                                                                                                                                                HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK
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                                                                            6; DB 5; ... 4e-167; ... 24; Indels
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84.7%; Pred. No. 4e-1
ive 43; Mismatches
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25-OCT-2001; 2001US-0342922P.
PEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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|QKLLKAYFEKLGVKNDF
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                                                                                               Similarity
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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Zamudio C, Trawick JD,

WPI; 2003-029926/02 N-PSDB; ACA47124 New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 25; SEQ ID NO 71178; 1766pp; English.

the 6213 antisenee sequences given in the specification where expression the 6213 antisenee sequences given in the specification where expression of the mucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid cacid encoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibitied by the artivity of a gene in an operon required for proliferation or the activity of a gene in an operon required for the proliferation, (7) identifying a compound that inhibits or proliferation; (8) required for proliferation, or that inhibits cellular proliferation (6) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or agene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound,'s activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to proliferation of an organism. The antisense uncleic acids required for cellular proliferation to isolate candidate molecules for rational dund iscovery programs, or for screening homologous mucleic acids required confidentifying proteins or screening for homologous mucleic acids required confidentifying proteins or screening for homologous mucleic acids required confidentifying proteins or screening for homologous mucleic acids required confident did not form part of the princed specification, but was obtained to the traget prokaryotic essential genes. Note: The sequence is encoded by one of the traget proferyor proliferation in cells other than S. aureus, S. typhimuring the call in electronic forma invention relates to an isolated nucleic acid comprising any

Sequence 437 AA;

WPI; 2003-029926/02.

N-PSDB; ACA22277

ö Gaps ö Length 437; IndelB 24; ; Pred. No. 4.9e-167; 43; Mismatches 24; 87.3%; Score 1985; DB 6; 84.7%; Matches 370; Conservative Best Local Similarity Query Match

120 1 MTHYHFVGIKGSGMSSLAQIMHDLGHBVQGSDIENYVFTEVALRNKGIKILPFDANNIKE DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 61 à 셤 8

HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180 121

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TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300 241

301 ETKVSNQVIVDDYAHHPREISATIETARKKYPQKDVVAVFQPHTFSRTQAFLNBFAESLS 360

ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNBFAESLS 360

301

361 KADQVFLCEIFGSIRENTGDLTIEDLINRIDGSTLIDENSIDVLEKFDNAVILFMGAGDI 420 Antisense; prokaryotic essential gene; cell proliferation; drug design. Zyskind JW; Xu HH; 361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI Ohlsen KL, Forsyth RA, Protein encoded by Prokaryotic essential gene #3934. Haselbeck R, Yamamoto R, ABU18407 standard; protein; 436 AA. Malone C, Carr GJ, 421 OKLONAYLDKLGMKNAF 437 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 06-MAR-2002; 2002US-0362699P. 21-MAR-2001; 2001US-00815242. 21-MAR-2002; 2002WO-US009107. 421 QKLLKAYFEKLGVKNDF (first entry) (ELIT-) ELITRA PHARM INC. Zamudio C, Trawick JD, Bacillus anthracis. WO200277183-A2 19-JUN-2003 03-OCT-2002 ABU18407; Wang L, Wall D, ABU18407 d 셤 à

the 6213 antisense sequences given in the specification where expression of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

Cf. (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concision acid in the specification of a polypeptide or its fragment whose expression is inhibited by the antisense concision acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway the gene product or that has an activity against a biological pathway in which a proliferation or that inhibits cellular proliferation; (8) identifying a gene required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprising strains in which the gene compound's activity; (11) a culture comprises or collection of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for identifying proteins or screening for homologous nucleic acids are useful for New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. invention relates to an isolated nucleic acid comprising any one of claim 25; SEQ ID NO 46331; 1766pp; English.

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for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                         121 HVMQCAHPISYLIGDGTGHGVENSKYFVFEACEYRRHFLSYNPDYAIMTNIDFDHPDYFT 180
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                                                                                                                                                                                                                              93;
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64.64; Score 1470; DB 6;
Best Local Similarity 64.74; Pred. No. 2.1e-121;
Matches 279; Conservative 59; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU29382 standard; protein; 445 AA.
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2001US-0342923P.
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2002US-0362699P.
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|| CKFEAAYVKEV 431
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                                                                                                                                                            Sequence 436 AA;
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06-SEP-2001; 2
25-OCT-2001; 2
08-FEB-2002; 2
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway concerning a gene product or that has an activity against a biological pathway of required for proliferation or the the test compound that inhibits ending retaining the pathway in which a proliferation or the broliferation or the brological pathway in which a proliferation required gene or its gene product lies or agene on which the test compound that inhibits apoliferation of an organism acts; (9) manufacturing an antibiotic; (10) prolification of an organism acts; (9) manufacturing an antibiotic; (10) prolification of an organism. The activity; (11) a culture comprising strains in which the gene product is overaxpressed or underexpressed; (12) determining the extent to broliferation of an organism. The antisense nucleic acids required for proliferation for an organism. The antisense nucleic acids required for cellular proliferation in cells other than S. aureus, S. typhimurium, X. premuoniae or P. aeruginosa. The present sequence is encoded by one of the target proxaryoric essential genes world. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the sequences.
                                                                                                                                                                                        New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303
                                                                                                                                                                                                                                                                                                                                 one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 VIAGNAFPDTHEBIARAIBLGAEVIRYHDFIARFIBPYTSIAVTGSHGKTSTTGLLAHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YHFVGIKGSGMSSLALVLAGKGYNVQGSDVEEYFFTQRDLEKSGVPILPFNADNIDKDMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 NGDKKTSFLIGDGTGMGLPBSDYFAFEACBYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                           Zyskind X
Xu HH;
                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid comprising any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.2%; Score 1438.5; DB 6; Length 445; 60.9%; Pred. No. 1.4e-118; ive 79; Mismatches 86; Indels 1;
                                                           ĀŞ
                                                             Ohlsen Forsyth
                                                             Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 57306; 1766pp; English
                                                             Malone C,
Carr GJ,
                    ELITRA PHARM INC.
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                                                             Zamudio C,
Trawick JD,
                                                                                                                               2003-029926/02
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                                                                                                                                                      N-PSDB; ACA33252
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Gaps ;

Length 436; Indels

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify.
363
                                                                  304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKAD
                                                      364 RVFLCEIFGSIRENTGALTIQDLIDKIE-GASLINEDSINVLEQFDNAVILFMGAGDIQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr GJ;
                                                                                                                                                                                                                                                                                                                  Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
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                                                                                                                                                                                                                                                                                         Enterococcus faecalis cellular proliferation protein #564.
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                                                                                                                                                                                                        AAU35277 standard; protein; 456 AA.
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25-MAY-2000; 2000US-0206848P.
25-MAY-2000; 2000US-020727P.
23-OCT-2000; 2000US-0242578P.
27-NOVY-2000; 200US-0253625P.
22-DEC-2000; 200US-025362P.
16-FEB-2001; 2001US-0269308P.
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                                                                                                                                                                                                                                                                (first entry)
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Xu HH;
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Yamamoto RT,
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20 YHFVGIKGSGMSSIALVLHQXGYNVQGSDVBEYFFTQRDLEKSGVPILPFNADNIDKDMI VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM

4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV

184 DVFDAFQEMAHNVKKGIIAWGDDEHLRKIRADVPIYYYGFKDSDDIYAQNIQITDKGTAF

200

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124 NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN

63 79

Gaps

1;

87;

DB 4; Length 456; Indels

63.0%; Score 1433.5; DB 4; 60.7%; Pred. No. 3.9e-118; ive 79; Mismatches 87;

Best Local Similarity bu. " Matches 258; Conservative

Query Match Best Local

Sequence 456 AA;

X S

380 EVFLCNIFGSARETQGEVRIEDLGEKIQKGGQVITEDNVSPLLDFENAEVVFMGAGDVQK 439

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364 RVFLCEIFGSIRENTGALTIQDLIDKIE-GASLINEDSINVLEQFDNAVILFMGAGDIQK

304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVEQPHTESRTQAFLNEFAESLSKAD

244 DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303

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design
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Xu HH;
                                                                                                                                                                                                                                                                                                                                            Antisense; prokaryotic essential gene; cell proliferation; drug
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Forsyth RA,
                                                                                                                                                                                                                                                              Protein encoded by Prokaryotic essential gene #15254
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Yamamoto R,
ABU29727 standard; protein; 444 AA.
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Carr GJ,
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06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
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                                                                                                                                                                               (first entry)
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Trawick JD,
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N-PSDB; ACA33597.
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                                                                                                                                                                               19-JUN-2003
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Wall D,
                                                                                       HANDER STANDARD BENEFIT OF STANDARD BENEFIT OF
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proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous of organisms. The present sequence for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fitp.wipo.int/pub/published_pct_sequences

screening New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs. New antisense nucleic acids, for homologous nucleic acids

Claim 25; SEQ ID NO 57651; 1766pp; English

the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter peperably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
encoding a polypeptide whose expression is inhibited by the antisense
comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
compression is inhibited by the antisense uncleic acid; (4) an antibody capable of specifically binding
the polypeptide (5) producing the polypeptide; (6) inhibiting cellular
compression or the activity of a gene in an operon required for
proliferation or that an antibody against a biological pathway
compounds agene required for cellular proliferation of the gene product lies
cor a gene on which the test compound that inhibits proliferation of an
compound's activity; (1) a culture comprising strains in which the gene
cor or a gene on which the test compound that inhibits in which the extent
compound's activity; (1) a culture comprising strains in which the extent
compound's activity; (1) a culture comprising strains in which the gene
cor or agene on which the test compound that inhibits the
compound's activity; (1) a culture comprising strains in which the
compound's activity; (1) a culture comprising strains in which the
compound is activity; (1) a culture comprising are useful for
compounds; or (13) identifying the target of a compound that inhibits the
compounds or screening for homologous nucleic acids required
cor dentifying proteins or screening for homologous nucleic acids required
cor dentifying proteins or screening for product milerational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumonnae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained The invention relates to an isolated nucleic acid comprising any one of n electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 444 AA;

Gaps 7 Length 444; 93; Indels 61.4%; Score 1396; DB 6; 60.6%; Pred. No. 7.9e-115; ive 74; Mismatches 93; Query Match 61.4% Best Local Similarity 60.6% Matches 260; Conservative ð

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Genomic sequence for Listeria monocytogenes, useful e.g. for treatment and prevention of Listeria and related bacterial infections, and related polypeptides.

WPI; 2002-010914/01.

Claim 6; SEQ ID NO 1467; 192pp; French.

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Dehoux P; Cossart P; Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P; Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart E Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA; Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A; Chakraborty T, Domann E, Hain T, Berche P, Charbit A, Durant L; Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N; Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J; Antibacterial, gene therapy; vaccine; biosynthesis; biodegradation; vitamin B12; bacterial infection; disease. Listeria monocytogenes protein #1466 ABB48762 standard; protein; 447 AA. 11-APR-2001; 2001WO-FR001118. 11-APR-2000; 2000FR-00004629. (first entry) Listeria monocytogenes : || :|| 428 FEOAY-EKL 435 423 LQNAYLDKL 431 (INSP) INST PASTEUR, Voss H; WO200177335-A2 05-FEB-2002 18-OCT-2001. Rose M, **ABB48762** à 셤

The present invention relates to the genome sequence of Listeria monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present invention Proteins expressed from the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific artipodies, identification of L. monocytogenes and related organisms, and for biosynthesis and biodegradation, especially biosynthesis of Vitamin B12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and modulate L. monocytogenes-related diseases. In addition, the genome sequence and proteins encoded by it are useful in pharmaceutical and vaccines compositions for the treatment or prevention of infections by L. monocytogenes and related organisms. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 447 AA;

. 0 Length 447; Indels 59.0%; Score 1342; DB 5; 59.7%; Pred. No. 4.9e-110; tive 64; Mismatches 108; Matches 255; Conservative Local Similarity Query Match

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1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120
                                  61 GLTIIAGNAFPDTHEEIERALELGLSVIRYHKFLGQLIDGYTSIAITGSHGKTSTTGLLS 120
                                                                                       181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
                                                                                                  241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300
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/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/foE_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5.1.6
Compugen Ltd
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US-09-540-286-2891
US-09-543-681A-5705
US-08-984-618-3
US-08-984-618-3
US-09-134-001C-3838
US-09-134-001C-3838
US-09-530-883-2
US-09-665-435A-2
US-08-643-309-2
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US-08-940-572-2
US-08-961-091-05
US-09-516-078-116
US-09-107-532A-6914
US-09-328-352-5023
US-09-489-039A-12280
US-09-252-991A-24196
US-09-252-991A-24196
US-09-198-452A-978
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US-09-198-452A-978
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US-09-147-928-2
US-09-134-001C-4284
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3-08-936-165A-446
3-08-934-481-2
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                                                                                                                                                                                                              389414 segs, 51625971 residues
GenCore version
Copyright (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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175.5 7.7 455 4 US-09-107-532A-5228 Sequence 522B, Ap 164.5 7.2 452 4 US-09-107-532A-5228 Sequence 6, Appli 160 7.0 335 3 US-08-961-083-10 Sequence 110, Appl 160 7.0 335 4 US-09-536-784-110 Sequence 110, Appl 160 7.0 451 4 US-09-536-784-110 Sequence 110, Appl 150 7.0 451 4 US-09-536-836-5 Sequence 7, Appli 150 6.9 483 4 US-09-184-918-2 Sequence 2, Appli 152 6.7 478 4 US-09-530-836-4 Sequence 4, Appli 151 6.6 419 4 US-09-540-236-3139 Sequence 12376, Appli 150.5 6.6 523 4 US-09-540-236-3139 Sequence 12376, Appli 160.5 523 4 US-09-540-236-3139 Sequence 7027, Appli 139.5 6.1 502 4 US-09-543-881A-7027 Sequence 7027, Appli 139.5 6.1 502 4 US-09-540-236-2593 Sequence 7027, Appli 135 5.9 463 4 US-09-540-236-2593 Sequence 7027, Appli 132.5 5.8 448 3 US-09-107-532A-7268 Sequence 7268, Appli 132.5 5.8 457 3 US-09-143-954-2 Sequence 2, Appli 132.5 5.8 457 3 US-09-143-954-2	ALIGNMENTS	RESULT 1 US-09-134-001C-5133 Sequence 5133, Application US/09134001C Sequence 5133, Application US/09134001C Sequence 5133, Application US/09134001C GENERAL INFORMATION: APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: WIGHER ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: DEPLERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS TURRENT APPLICATION NUMBER: US 60/05/134,001C CURRENT APPLICATION NUMBER: US 60/064,964 PRIOR APPLICATION NUMBER: US 60/065,779 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR PILING DATE: 1997-08-14 SEQ ID NO 5133 LENGTH: 442 LENGTH: 442 TYPE: PRT ORGANISM: Staphylococcus epidermidis US-09-134-001C-5133	y Match 87.3%; Score 1986; DB 4; Length 442; Local Similarity 84.7%; Pred. No. 1.1e-185; hes 370; Conservative 43; Mismatches 24; Indels 0; Gaps 0;	MTHYHFVQIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE	6 MTHYHEVGIKGSGMSSLAQIMHDLGHEVQGSDIESYVFTEVALRNKGIKILPFDANNITK 65 61 DMVVIQGNAFASSHEBIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120	:	121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180 	181 DINDVPDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240 : : :
22883333333333333333333333333333333333		RESULT 1 US-09-134- ; Sequence ; Patent N GENERAL ; APPLICA ; TITLE O TITLE O ; TITLE C ; TITLE N ; FILE RE ; CURRENT ; FURENT ; FRIOR F ; PRIOR F	Query Match Best Local Matches 37	<i>\delta</i> 1	8 8	i A	රු පි	<i>₹</i> 6

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125 ISHITDTSFLIGDGTGRGSANAKYFVFESDEYERHFMPYHFEYSIITNIDFDHPDYFTSL 184
                                                                                                                     183 NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGT 241
                                                                                                                                                                                                                                                                                                                                                                                             302 TIIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSK 361
                                                                                                                                                                                                                                                         242 AFDVYVDGEFYDHFLSPQYGDHTVLNALAVIALSYLEKLDVTNIKEALETFGGVKRRFNE 301
                                                                                                                                                                                                                                                                                                                                                                                                                                        305 XIVNDTVIIDDFAHHFTEIIATLDAARQKYPSKEIVAVFQPHTFTRTIALLDDFAHAINQ 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                    185 EDVFNAFNDYAKQITKGLFVYGEDAELRKITSDAPIYYYGFEAEGNDFVASDLLRSTTGS
                                                                                                                                                                                                                                                                                                    245 TFTVHERGQNLGQFHIPTFGRHNIMNATAVIGLLYTAGFDLNLVREHLKTFAGVKRRFTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 ADRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGD
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APPLICANT: Choi et. al.
APPLICANT: Choi et. al.
ITILE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEB: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.8%; Score 1043; DB 3; Length 422; Best Local Similarity 48.8%; Pred. No. 1.7e-93; Matches 200; Conservative 80; Mismatches 126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BICOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ IB NO: 116:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
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Patent No. 6159469
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425 IQTYEYSF 432
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STRANDEDNESS: si
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361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 420
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                                          366 KADQVFLCEIFGSIRENTGDLTIEDLINRIDGSTLIDENSIDVLEKFDNAVILFMGAGDI
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Best Local Similarity 49.8%; Pred. No. 7e-101;
Matches 213; Conservative 84; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wallis, Nicola G.
APPLICANT: Black, Michael T.
APPLICANT: Hodgson, John E.
APPLICANT: Knowles, David J.
APPLICANT: Lonetto, Michael A.
APPLICANT: Nicholas, Richard O.
APPLICANT: Steddia, Robert K.
TITLE OF INVENTION: No. 6310193el Murc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 08-7UL-1997
ATTOMACE: 08-7UL
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/08940572
Patent No. 6310193
                                                                                                                                           OKLONAYLDKLGMKNAF 437
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OKLLKAYFEKLGVKNDF 442
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ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 215/994-2222
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APPLICANT: Wallis,
APPLICANT: Black,
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CLASSIFICATION:
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Gaps

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Mismatches 126; Indels

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200; Conservative
           Matches
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                                                                                                                                                                                                                                                      121 SANAKYFVFESDEYERHFMPYHPEYSIITNIDFDHPDYFTSLEDVFNAFNDYAKQITKGL 180
                                                                                                                                                                                                                                                                                                                                                                                                    260 YGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPRE 319
                                                                                                                                                                                                                                                                                                                                                               201 IAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQ 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 ISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRE-NT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | ||:: ||:|| ||:|||||:|||||:|| ||::|| ||::|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:
           9
                                                                                                                   Sequence 116, Application US/09536784
Patent No. 6573082
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
   HOMGHKVOGSDVEKYYFTORGLEQAGITILPFDEKNLDGDMEIIAGNAFRPDNNVEIAYA
                                                                                                                                                                                                                 141 LPBSDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGI
                                                                      81 HQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GALTIODLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIOKLONAY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1043; DB 4; Length 422;
Pred. No. 1.7e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DESCRIPTION: SEQ ID NO: 116
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TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 422 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (301) 309-8512
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48.8%;
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
ULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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Best Local Similarity
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US-09-536-784-116
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SEQUENCE
US-09-536-784-116
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECTUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                   140
                                                                                                                                61 DONGISYKRYHBFLGSFWRDFVSMGVAGAHGKTSTTGMLSHVLSHITDTSFLIGDGTGR 120
                                                                                                                                                                                                     200
                                                                                                                                                                                                                       121 SANAKYFVESDEYERHFMPYHPEYSIITNIDFDHPDYFTSLEDVFNAFNDYAKQITKGL 180
                                                                                                                                                                                                                                                                                                                        300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 ISATIETARKKYPHKEVVAVFOPHTFSRTQAFINEFAESLSKADRVFLCEIFGSIRE-NT 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                   9
                            22 HDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMVVIQGNAF-ASSHEEIVRA
                                                                                            81 HQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMG
                                                                                                                                                                                                                                                                                                                                                                                                260 YGDHTVINALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPRE
                                                                                                                                                                                                                                                                                                                                                                                                                            241 FGRHNIMMATAVIGLLYTAGFDLNLVREHLKTFRGVKRRFTEKIVNDTVIIDDFAHHPTE
                                                                                                                                                                                             141 LPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               379 GALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQKLQNAY 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: PC
COMPUTER: PC
CORRENTING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6914, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD/ROM ISO9660
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COUNTRY: USA
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COMPUTER READABLE FORM:
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Sequence 2712.7. Application US/09540236

Sequence 2712.7. Application US/09540236

Patent No. 6673910

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAI TITLE OF INVENTION: ROR DIAGANSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
UNRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

SEQ ID NO 2712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----QAVDVIADGT-KTHFTVLRKDKKPLPITLNIPGIHNVYNALGAITMATDEGV 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RILYMMEQPHRYSRIRDCFSEFVNVLSQVDKLILLDVYSAGEELIKGATSNDLARSLRBR 440
273 AIDVEQDGMRSHFTVLRKGREPLRLTINQPGLHNVLNALAAIGVATDGGVSDEAISRALK 332
                                                                                                                                                 391
                                                                                                                                                                       64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 DVTNIKEALETFGGVKRRFNET-----TIANQVIVDDYAHHPREISATIETARKKYPH 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 KEVVAVFOPHTFSRTOAFINEFAESISKADRVFLCEIFGSIRENTGALTIODLIDKIBGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                 291 TFGGVKRRFN-----ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTF
                                                                                       333 GFSGVGRRFQVQGEFELGEGNVKLVDDYGHHPKEVEATIKAARQSHPDRRLVWLFQPHRY
                                                                                                                                                     346 SRIQAFINEFAESISKADRVFLCEIFGS-----IRENIGALTIQ-----DLIDKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 HFVGIGGAGMCGIAEVLANQGYVVTGSDIKANAMTE-RLENLGVTVHVGHDASNIKMADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.4%; Score 532; DB 4; Li
32.1%; Pred. No. 2.2e-43;
ive 78; Mismatches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 SLINEDSINV--LEQFDNAVILFMGAGDIQKLQNA 426
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                                                                                                                                                                                                                                      392 GASLINEDSI -- NVLEQFDNAVILFMGAGDI 420
                                                                                                                                                                                                                                                               453 G----NLQNIMQNVLQ--PNDLLLTQGAGNV 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.1%
Matches 146; Conservative
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ORGANISM: M.catarrhalis

US-09-540-236-2712
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US-09-489-039A-12280
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US-09-328-352-5023
Sequence 5023, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNMERR: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD-YFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADV--PIYYYGFKDSDDIY 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGVRPISYLIGDGTGHGDPQAEFFSFEACEYRRFILAYSPDYAIMTNIDFDHPDYYTSID 192
                                                                                                                                                                                                                                                                                                                                                                                              NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTAF 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
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                                                                                                                                                                                                                                                                                                             13 YHFVGIKGSGMSSLALVLHEQGLNVQGSDIEKYFTQRDLEKANITILPFNADNVKPGMT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 HIHFVGIGGAGMCGIAEVLANQGYKISGSDIKASKTTQ-QLEENGIKVYIGHEAENIKNA
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                                                                                                                                                                                                 Length 291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Mismatches 171;
                                                                                                                                                                                                   42.5%; Score 967; DB 4; llarity 63.8%; Pred. No. 2.7e-86; Conservative 43; Mismatches 58
                                                                            ;
NAME/KEY: misc_feature
;
LOCATION: (B) LOCATION 1...291
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SEQUENCE DESCRIPTION: SEQ ID NO: 6914:
US-09-107-532A-6914
                                                    ORGANISM: Enterococcus faecium
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Matches 154; Conservative
             HYPOTHETICAL: YES
                                ORIGINAL SOURCE:
                                                                                                                                                                                                                     Local Similarity
les 178; Conserv
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US-09-328-352-5023
                                                                          FEATURE
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Matches
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; TYPE: PRT
; ORCANISM: Pseudomonas aeruginosa
US-09-252-991A-24196
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           Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12280
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196_136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER: OS 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24196
LENGTH: 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 KEALETFGGVKRRFN---ETTIA-----NQVIVDDYAHHPREISATIETARKKYPHKE 335
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                                                                                                                                                                                                                                                                                                                      21.9%; Score 499; DB 4; Length 492; 30.0%; Pred. No. 3.6e-40; Live 86; Mismatches 192; Indels
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Sequence 12280, Application US/09489039A
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Matches 137; Conservative
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GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 1900-04-05
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
                                                                                                                                              64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                          124 -NGDKKTSFLIGD-----GTGMGLPESDYFAFRACEYRRHFLSYKPDYAIMTNIDFDH-P 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 TNIKBALETFGGVKRRFN----ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    341 RAIVQGLSGFQGVGRRFQVYGELQVEGGSVMLVDDYGHHPREVAAVIKAIRGGWPERRLV 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 EDSINVLEQFDNA-----VILFMGAGDI----QKLQNAYLDKLGMKNA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         460 -DPIYFERDADLAPLUXPILRAGDILLCQGAGDVGGLAPQLIKNPLFAGKGGKGA 513
                                                                 26;
     Length 513;
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Query Match
21.5%; Score 490; DB 4; Length 51;
Best Local Similarity 30.9%; Pred. No. 2.9e-39;
Matches 147; Conservative 77; Mismatches 195; Indels
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20.9%; Score 475; DB 4; Li
Best Local Similarity 28.0%; Pred. No. 8e-38;
Matches 132; Conservative 86; Mismatches 183;
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Patent No. 6605709
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APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFITIE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
                                                                                                                                                                                                                                                                                                       Sequence 4942, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
FOR INVENTION:
FOR INVENTION:
FILE OF INVENTION:
FILE REFERENCE: 6TC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
         345 IRRVIAIFQPHRFSRLEECLQTFPKAFQEADEVILTDVYSAGESPRESIILSDLAEQIRK 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSHVMN-GDKKTSFLIGDGTGMGLPES-----DYFAFEACEY------RRHFLSYKPD 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 YYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEK 279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 YAIMTNIDFDHPDYFKDINDVFDAFQEMAHNV--KKGIIAWGDDEHLRKI---EADVPIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 RISLEANEKAALSAELISIDGSHFKVLENGNVIGEVKWSMTGQHSVANALATIAAAQHVG
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                                                                                                                                          393 ASLI-----NEDSINVLEOF--DNAVILFMGAGDIOKLONAYLD
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Patent No. 6673910
GENERAL INFORMATION:
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Best Local Similarity 29.2%
Matches 135; Conservative
                                                                                                                                                                                                                                                          RESULT 12
US-09-328-352-4942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: ACLIR
US-09-328-352-4942
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Batent No. 65529294
GENERAL INFORMATION:
APPLICANT: Griffale, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
CURRENT APPLICATION NUMBER: US/09/199,452A
CURRENT APPLICATION DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                           ---MNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNID 172
                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                    SEDADVRITHYE--QKGAQGFFTISREDMPDIDVVLNAP-----GRHNALNATAA 301
                                                                                                                                                                                                                                                                                                                                                                 272 IAISYLEKLDVINIKEALETFGGVKRRFN------ETTIANQVIVDDYAHHPREIS 321
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                                                      142 YAQAGLDPTFVNG----GLVKSAĞTHARLGCSRYLIAEADESDASFLHLQPMVAVVTNIE
                                                                                                                                                                                                                                                 -----FDVYVDGEFYDHFLSPQYGDHTVLNALAV
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                                                                                                                                                             ADHMDIYHGNFDNLKETFITFLHNLP----FYGRAVMCIDDDVIRSIIPKVGRYITTYGF
                                                                                                                       FDHPD-YFKDINDVFDAFQEMAHNVKKGIIAWG-----DDEHLRKIEADVPIYY--YGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKADRVFLCEIFGS-----
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28.2%; Pred. No. 5.5e-37;
tive 89; Mismatches 181; Indels
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Sequence 100 Application US/09489039A

Sequence 8610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/489,039A

CURRENT APPLICATION NUMBER: US/09/489,039A

CRRENT APPLICATION NUMBER: US 60/117,747

PRIOR SEQ ID NOS: 14342

SEQ ID NO 8987
                                                                                                                                        60 EDMVVIQGNAFASSHERIVRAHQLKLDVVSYNDFL-GQIIDQYTSVAVTGAHGKTSTTGL 118
                                                                                                                                                                                LSHVMNG-DKKTSFLIGDGTG-----MGLPESDYFAFEACEY------RRHFLSYKPDY 165
                                                                                                                                                                                                                                                                                                                   LAWILEDCGYOPGFLIGGVPGNFQVSAQLGESPFFVIRADEYDSAFFDKRSKFVHYSPRT 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 L-AVIAISYLEKUDVINIKEALETFGGVKRRFNETTIANQV-IVDDYAHHPREISATIET 326
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                     HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNIK-- 59
                                                          14 HIHILGICGTFWGSLAILARAKGHKVTGSDANVYPPMSTLLENQGIELIEGYDPQQLEPA 73
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193 LILMNLEPDHADIFDDLTAIQXQFHHLVRIVPGSGKIIMPDNDLNLKQTIGMGCWSEEE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         327 ARKKY-PHKEVVAVFOPHTFSRTGAF-LNEFAESLSKADRVFL 367
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Best Local Similarity 27.2*
Matches 129; Conservative
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US-09-489-039A-8987
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Batent NO. 6665705.

Batent NO. 6665705.

Batent NO. 6665705.

BAPLICANT: GARY BERTON

TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL

TITLE OF INVENTION: DAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

PRIOR FILING DATE: 1999-04-09

SEQ ID NO 5765

SEQ ID NO 5765

LENGTH: 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --RRHFLSYKPDYALMTNIDFDHPDYFKDINDVFDAFQEMAHNV-KKGIIAWGDDEHLRK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----FYD 253
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                                                                                                                                                                                                                                                                                                                                                              3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILP-FDANNI--K 59
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                     DB 4; Length 473
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                                                                                                                                                                                                                                        Query Match
17.0%; Score 386.5; DB 4; Length
Best Local Similarity 27.8%; Pred. No. 3.5e-29;
Matches 136; Conservative 82; Mismatches 177; Indels
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CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2891
LENGTH: 473
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US-09-540-236-2891
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Search completed: June 3, 2004, 14:41:12 Job time: 23 secs

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1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVPTEVALRNKGIKILPPDANNIKE
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Best Local Similarity 100.
Matches 437; Conservative
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Sequence 2, Appli
Sequence 43780, A
                                                                                                                              3, 2004, 14:40:41; Search time 48 Seconds (without alignments) 2561.354 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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6 US-10-712-713-2

2 US-10-282-122A-43780

US-09-815-242-12293

US-10-282-122A-71178

2 US-10-282-122A-46331

US-10-282-122A-46331

US-09-815-242-10870

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US-09-815-242-10870

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Maximum Match 100%
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CURRENT APPLICATION NUMBER: US/09/925,637

FRICH PAPLICATION NUMBER: PCT/US00/23773

FRICH REPLICATION NUMBER: PCT/US00/23773

FRICH REPLICATION NUMBER: US 60/151,933

FRICH FILING DATE: 1999-09-01

FRICH REPLICATION NUMBER: US 60/151,933

FRICH FILING DATE: 1997-01-03

FRICH REPLICATION NUMBER: US 08/956,171

FRICH REPLICATION NUMBER: US 60/009,861

FRICH REPLICATION NUMBER: US 60/009,861
                                    Sequence 71315, A
Sequence 51682, A
Sequence 51682, A
Sequence 51682, A
Sequence 61427, A
Sequence 61427, A
Sequence 6151, A
Sequence 6121, A
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Sequence 5131, A
Sequence 5131, A
Sequence 5131, A
Sequence 51682, A
Sequence 51313, A
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Sequence 5183, A
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US-10-282-122A-44665
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Patent NO. US20020103338A1
GENERAL INFORMATION:
APPLICANT: Choi
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301 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS 360
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; Publication No. US20040082002A1
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil
; TITLE OF INVENTION:
; FILE REFERENCE: PESIST:
; CURRENT APPLICATION NUMBER: US/10/712,713
; CURRENT ALING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: PCT/US00/23773
; PRIOR PELING DATE: 2000-08-31
; PRIOR PILING DATE: 2000-08-31
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 3.1
; SEQ ID NO 2
; LENGTH 437
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; Sequence 2, Application US/10084205
; CENERAL INFORMATION:
; APPLICANT: Choi, Gil
TITLE OF INVENTION: 37 Staphylococcus aureus Genes and Polypeptides
; TILE APPLICATION UNMBER: US/10/084,205
; CURRENT APPLICATION NUMBER: US/10/084,205
; CURRENT APPLICATION NUMBER: CIT/US00/23773
; PRIOR FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2000-08-31
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PATENTIN Ver. 3.1
; SOFTWARE: PATENTIN Ver. 3.1
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Query Match

100.0%; Score 2275; DB 14; Length 437;

Best Local Similarity 100.0%; Pred. No. 2.9e-198;

Matches 437; Conservative 0; Mismatches 0; Indels 0;
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241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300
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                                                                                                 301 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLS
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APPLICANT: Yanamoto, Robert T.

APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PLING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR FILING DATE: 2000-11-27

PRIOR PRILING DATE: 2000-11-27

PRIOR PRILING DATE: 2000-11-27

PRIOR PRILING DATE: 2000-12-22

PRIOR PRILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SEQ ID NO SEQ ID NOS: 14110

SEQ ID NO SEQ ID

LENGTH. 437
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99.5%; Pred. No. 1.6e-197;
live. 1; Mismatches 1;
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Patent No. US20020061569A1
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US-09-815-242-5297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ohlsen, Kari I.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
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Best Local Similarity 99.53
Matches 435; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: FORSYTH, R. APPLICANT: YOUNGED.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITEA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRIOR FILING DATE: 2000-05-28

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-01-0-23

PRIOR FILING DATE: 2000-10-23

PRIOR PRILING DATE: 2000-10-23

PRIOR PRILING DATE: 2000-11-23

PRIOR PRILING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-22

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR PLING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-06

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-09
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                                                                                 Sequence 43780, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: ABelbeck, Robert
APPLICANT: ABelbeck, Robert
APPLICANT: Cyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yensyth, R.
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Best Local Similarity
Matches 436; Conserv
                                                         US-10-282-122A-43780
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APPLICAMY: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/203
PRIOR PILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/203
PRIOR PILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PILING DATE: 2001-02-09
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128 HVWNGDXKTSFLIGDGTGMGLPESDYFAFBACEYRRHFLSYKPDYAIMTNIDFDHFDYFK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI 420
                                                                                                                                                                                                                               248 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
                                                                                                                                                                                                                                                                                                                                                                     308 ETTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFINEFAESLS
                                                                                                                    188 DINDVPDARQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
                                                                                                                                                                                            241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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                                                                 181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG
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US-10-282-122A-71178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
SEQ ID NO 71178
LENGTH: 437
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DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
                                                                                                      241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIALSYLEKLDVINIKEALETFGGVKRRFN 300
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APPLICANT: Oblsen, Kari L.

APPLICANT: Transion, Judith W.

APPLICANT: Transion, Judith W.

APPLICANT: Transion, Judith W.

APPLICANT: Transion, Judith W.

APPLICANT: Transco, John D.

APPLICANT: Transco, Robert T.

APPLICANT: Xu, Howard

TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: UNMBER: US/09/815,242

CURRENT APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-01-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2000-11-27
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Pred. No. 1.6e-197;
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Patent No. US20020061569A1
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US-09-815-242-12293
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Best Local Similarity 99.5%;
Matches 435; Conservative
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APPLICANT: Haselbeck, Robert
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US-09-815-242-12293
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LENGTH: 444
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ORGANISM:
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PRIOR APPLICATION NUMBER: 60/191,078
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Chlsen, Kari
APPLICANT: Syskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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Yamamoto, Robert
Forsyth, R.
           FILING DATE: 2000-12-22
                                                                                                                                                                                                       ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                             Best Local Similarity 64.7
Matches 279; Conservative
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OKFEAAYVKEV 431
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APPLICANT:
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APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yamamoto, Robert
APPLICANT: Yorsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITAR.034
CURRENT PELING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-11-27
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                                                                                                                                                61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS
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                                            Gaps
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       Length 437;
                                          Indels
     87.3%; Score 1985; DB 12;
84.7%; Pred. No. 7.3e-172;
iive 43; Mismatches 24;
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Publication No. US20040029129A1
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421 QKLLKAYFEKLGVKNDF 437
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APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olleen, Kari
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                          Conservative
Query Match
Best Local Similarity
Matches 370; Conserv
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US-10-282-122A-46331
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APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELLITA.034A
CURRENT APPLICATION VMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
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PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 46331
LENGTH: 436
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                                                                                                                                                                                                                                                                                                                                                Length 436;
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64.7%; Pred. No. 5.4e-125;
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                                                                                                                                                                                                                                                                                                                                                                                                   59; Mismatches
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80 VIAGNAFPDTHEELARAIELGAEVIRYHDFIARFIEPYTSIAVTGSHGKTSTTGLLAHVL 139
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                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Protection of Essential Genes in TITLE OF INVENTION: Protection of Essential Genes in TITLE OF INVENTION: PRIOR APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00/10-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-25
PRIOR FILING DATE: 2000-05-26
PRIOR PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR APPLICATION NUMBER: 60/24,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/253,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 63.0%; Score 1433.5; DB 9; Best Local Similarity 60.7%; Pred. No. 1.2e-121; Matches 258; Conservative 79; Mismatches 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10870
LENGTH: 456
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US-10-282-122A-57651
; Sequence 57651, Application US/10282122A
; Publication No. US20040029129A1
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                                                                                               Yamamoto, Robert T.
                                           Trawick, John D. Carr, Grant J.
                   Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM NUMBER OF SEQ ID NOS: 78614 SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 12; Length 445;
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60.9%; Pred. No. 4.1e-122;
tive 79; Mismatches 86;
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR PAPPLICATION NUMBER: 60/207, 727
PRIOR PAPPLICATION NUMBER: 60/200, 335
PRIOR PAPPLICATION NUMBER: 60/200, 347
PRIOR PILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242, 578
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-12-22
PRIOR FILING DATE: 2001-02-05
PRIOR FILING DATE: 2001-02-06
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Patent No. USJ0020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari I.
APPLICANT: Zyskind, Judith W.
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LENGTH: 445
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Best Local Simi
Matches 259;
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APPLICANT: Xu, H.,

TITLE OF INVENTION: Identification of Essential Genes in Microcrganisms
FILE REPERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-66
PRIOR PILING DATE: 2000-05-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-010-23
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2001-02-09
                                         364 RVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQK 422
                                                                           61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120
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NUMBER OF SEQ ID NOS: 78614
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 60988, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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ORGANISM: Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Simi:
Matches 255;
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/206,848

PRIOR PILING DATE: 2000-05-28

FRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

FRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR PRILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR PRILING DATE: 2000-12-27

PRIOR PILING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
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US-10-282-122A-57651
                              Mang, Liangsu
Zamudio, Carlos
Malone, Carlos
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
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SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                              Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 60.6*
Matches 260; Conservative
SENERAL INFORMATION
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APPLICANT:
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Query Match
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APPLICANT:
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APPLICANT: Anamanco, Robert
APPLICANT: Yu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PLING DATE: 2000-03-21
PRIOR PLING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/200,727
PRIOR PLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-10-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-23
PRIOR PLING DATE: 2000-110-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-06
181 DINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
                                                                                                                                                                        241 TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300
                                                                                                                                                                                                      241 TKFDVYHREEFLSSFEIPAYGDHNVLNALSVIALCDYEGLPVEDVKNELKTFEGVKRRFS 300
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SOFTWARE: PatentIn version 3.1
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Publication No. US20040029129A1
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; ORGANISM: Streptococcus pyogenes
US-10-282-122A-74395
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APPLICANT: Wang, Liangsu
APPLICANT: Tamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Othern, Rari
APPLICANT: Othern, Rari
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Travick, John
APPLICANT: Trawick, John
APPLICANT: Tamanoto, Robert
APPLICANT: Forgyth, R.
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                                                                                                                                            5 YHFIGIKGSGMSALALMLHQMGHKVQGSDVEKYYFTQRGLEQAGITILPFSEDNITPDME
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                                                       Gaps
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     Length
                                                       Indels
50.1%; Score 1139; DB 12;
50.7%; Pred. No. 7.4e-95;
iive 82; Mismatches 128;
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR APPLICATION NUMBER: 60/245,578
PRIOR PILING DATE: 2000-11-23
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Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Samudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
                                                    Matches 218; Conservative
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6 HFIGIKGSGMSALALLLHQWGYKVQGSDVDKYYFTQHGLEKAGIPILPFAESNITNDMBI
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                                                                                                                                                                                                                                                                                                                                              3; Gaps
                                                                                                                             or PALM
                                                                                                                                                                                                                                                                                                         Length 443;
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR PILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper of Software: Patentin version 3.1
SEQ ID NO 72179
LENGTH: 443
                                                                                                                                                                                                                                                                                                     Query Match 49.8%; Score 1132.5; DB 12; Lengt
Best Local Similarity 50.7%; Pred. No. 2.9e-94;
Matches 218; Conservative 84; Mismatches 125; Indels
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APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
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Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari L.
                                                                                                                                                                                                                                       ORGANISM: Streptococcus mutans
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426 LYERSFEELL 435
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64 VIQGNAF-ASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
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Best Local Similarity 49.8%; Pred. No. 4.9e-93;
Matches 213; Conservative 84; Mismatches 127;
            PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-110-23
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRANKO FOR SEXEND FOR SECOND NOS: 14110
SECOND NO 13507
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; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13507
FILING DATE: 2000-05-23
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UDP-N-acetylmurama
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                                                           3, 2004, 14:38:01; Search time 20 Seconds (without alignments) 2101.785 Million cell updates/sec
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Compugen Ltd.
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GenCore version
Copyright (c) 1993 - 2004
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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UDP-N-acetylmurama UDP-N-acetylmurama probable muramate- probable unp-N-ace UDP-N-acetylmurama	ALIGNMENTS Limported] - Staphylococcus aureus (strain N315) on 10-May-2001 #text_change 22-Oct-2001 ; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; ra, N.; Hayashi, H.; Hiramatsu, K. meticillin-resistant Stapylococcus aureus. 11952; PMID:11418146 sgl3701535; PIDN:BAB42829.1; GSPDB:GN001499 alanine ligase	100.0%; Score 2274; DB 2; Length 437; imilarity 99.8%; Pred. No. 1.4e-148; ; Conservative 1; Mismatches 0; Indels 0; Gaps 0; MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENTVFTEVALRNKGIKILPFDANNIKE 60 MINTYLEVGIKGSGMSSLAQIMHDLGHEVQGSDIENTVFTEVALRNKGIKILPFDANNIKE 60 DMVVIQGNAFASSHEETVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120 MINTYLGANFASSHEETVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120 HVMNGDKKTSFLIGGGTGMGLPESDYFAPEACEYRHFLSYKPDYAIMTNIDFDHPDYFK 180 HVMNGDKKTSFLIGGGTGMGLPESDYFAPEACEYRHFLSYKPDYAIMTNIDFDHPDYFK 180 DINDVFDAFQEMAHVVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240 DINDVFDAFQEMAHNVKKGIIAMGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKG 240
A10068 A72402 A72402 A72402 B64185 D82081 C81308 C84955 D70579 D70579 B71917 G64002	ramate-alanine ligase [import hylococcus aureus 2001 #sequence_revision_10=140 2958	imilarity 99.8%; Pred. No.; Conservative 1; Mismat. Conservative 1; Mismat. MTHYHFVGIKGSGWSSLAQIMHDLGHEVQ
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4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	e-alanine lig occus aureus #sequence_rev T.; Uchiyama, Y.; Kobayash O. 2001, M.; Ogas O. 2001 e sequencing A89758; MUD: Y UR> GB:BA000018; e: strain N31	100.0%; ty 99.8%; 99.8%; GIKGSGMSSLAK
60000000000000000000000000000000000000	ramate-a hylococc 9501 #89 9501 #1-U1, Y. H-U1, Y. 1-U1, Y. 5-1240, 5-1240, 6-1240, 3-	Similarity 6; Conser MTHYHFVGI MTH/H MTH/H MTH/H MTH/H MTH/H MTH/H DMVVIQGNA HVMNGDKKT DINDVFDAF
444 4 4 4 6 600 0 4 4 1 0 4441004 W4147449W 600	RESULT 1 H89958 UDP-N-Aacerylmuramate-alanine 1 C; Species: Staphylococcus aureu C; Deccies: 10-May-2001 #sequence_r C; Date: 10-May-2001 #sequence_r C; Accession: H89958 R; Kuroda, M.; Ohta, T.; Uchiyam ma, A.; Mizutant-Ui, Y.; Kobaya C.; Shiba, T.; Hattori, M.; Og Lancet 357, 1225-1240, 2001 A; Title: Whole genome sequencin A; Atterence number: A89758; MUI. A; Accession: H89958 A; Status: preliminary A; Status: 1-437 *KUR> A; Cross references: GB:BA000018 A; Cross references: GB:BA000018 A; Cross references: GB:BA000018 A; Cross references: GB:BA000018 A; Genetics: A; Genetics: C; Superfamily: UDP-N-acetylmuran	atch cal S 436 436 11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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TAPDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN 300

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KADRVFLCEI FGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVILFMGAGDI

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CyAccession: H84055
RyTakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirz
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: H84055
A;Accession: H84055
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 - SSTO>
A;Accession: 1-433 - SSTO>
A;Accession: 1-433 - SSTO>
A;Accession: 1-433 - SSTO>
A;Accession: 1-432 - STO>
A;Experimental source: strain C-125
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241 TTFDVFVRNTFYDTFYIPAYGHHNVLNSLAVIALCHYEEIDSSIIKHALKSFGGVKRRFN 300
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C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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Matches 253; Conservative
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A;Status: production acid sequence not shown; translation not shown
A;Status: production of shown
A;Residues: 1-432 <KUN>
A;Residues: 1-432 <KUN>
A;Cross-references GB:299119; GB:AL009126; NID:g2635411; PIDN:CAB14957.1; PID:g2635463
A;Experimental source: strain 168
R;Varon, D; Brody, M.S.; Price, C.W.
Mol. Microbiol. 20, 339-350, 1996
A;Title: Bacillus subtilis operon under the dual control of the general stress transcrip
A;Reference number: S71000; MUID:96310371; PMID:8733232
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C,Superfamily: UDP-N-acetylmuramate-alanine ligase
C,Keywords: ATP binding; cell division; cell wall; ligase; peptidoglycan biosynthesis
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361 KADRVFLCEIFGSIRENTGALTIQDLIDKIEGASLINEDSINVLEQFDNAVVLFMGAGDI 420
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A;Reaidues: 85-432 - CVAR>
A;Cross-references: EMB:L31845; NID:g556013; PIDN:AAB40043.1; PID:g556014
A;Experimental source: strain 168, substrain Marburg
                                                                                                                                                                                                                                                         C69662
UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) murc - Bacillus subtilis
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A; Accession: AE1275
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-447 cGLA>
A; Cross-references: GB:NC_003210; PIDN:CAC99683.1; PID:g16411034; GSPDB:GN00177
A; Experimental source: strain RGD-e
C; Genetics:
A; Genetics:
A; Genetics: C; Superfamily: UDP-N-acetylmuramate-alanine ligase
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
59.0%; Score 1342; DB 2; Length 4
Best Local Similarity 59.7%; Pred. No. 1.4e-84;
Matches 255; Conservative 64; Mismatches 108; Indels
A; Reference number: AB1077; MUID:21537279; PMID:11679669
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C,Superfamily: UDP-N-acetylmuramate-alanine ligase
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C;Dacession: AE1275
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
J; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Title: Comparative genomics of Listeria species.
                                                                         Cipecies: Listeria innocua
Cipecies: Listeria innocua
Cipecies: Listeria innocua
Cipecies: Trov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Cipate: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
Cipate: 27-Nov-2001
Cipate: 27-Nov-2001
Cipate: Cipat
                                             UDP-N-acetyl muramate-alanine ligases homolog murc [imported] - Listeria innocua (strain
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A;Experimental source: strain Clip11262
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Best Local Similarity 60.23
Matches 257; Conservative
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nocological protein murC [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C; Species: Lactococcus lactis subsp. lactis (c; Species: Lactococcus lactis subsp. lactis H86879 lactorin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Bhrlit Genome Res. 11, 731-753, 2001 lactic acid bacterium Lactococcus lactis ssp. A, Atitle: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. A, Accession: H86879 lactis lactis sp. A, Accession: H86879 lactis l
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C.Species: Streptococcus pneumoniae
C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C;Accession: B95177
R;Tettelin, H:; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Aterence number: A95000; MUID:21357209; PMID:11463916
A;Accession: B95177
A;Accession: 
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A;Experimental source: strain TIGR4
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                                                                                                                         245 TFTVHFRGQNLGQFHIPTFGRHNIMMATAVIGLLYTAGFDLNLVREHLKTFAGVKRRFTE
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185 EDVFNAFNDYAKQITKGLFVYGEDAELRKITSDAPIYYYGFEAEGNDFVASDLLRSTTGS
                                                                             242 APDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNE
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A;Gene: SP1521
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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R,Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; E. R.; LeBlanc, D.J.; Lee, L.W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; E. R.; LeBlanc, D.J.; Lee, L.W.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; J.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A,Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R. A;Reference number: A97872; WuID:21429245; PMID:11544234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8) [imported] - Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VIQGNAF-ASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 MNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRFFLSYKPDYAIMTNIDFDHPDYFKDI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHITDTSFLIGDGTGRGSANAXYFVFESDEYERHFMPYHPEYSIITNIDFDHPDYFTSL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFK-DSDDIYAQNIQITDKGT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420
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                                                                                                                                                                                                                                                                                                                                                                                            198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          303 TIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFINEFAESISKA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 KVGETVIIDDPAHHPTEIEATLDAARQKYPDREIVAVFQPHTFTRTIAFADEFAEVLDHA 378
                                                                                                                                                                                         MNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNET 302
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C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 YHFIGIKGSGMSALALMLHQMGHKVQGSDVEKYYFTQRGLEQAGITILPFDEKNLDGDME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                          VIQGNAFASSHE-EIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV
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49.2%; Score 1119; DB 2; Length 444;
Best Local Similarity 49.8%; Pred. No. 2.8e-69;
Matches 213; Conservative 84; Mismatches 127; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: UDP-N-acetylmuramate-alanine ligase
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OKYELAF-EKL 448
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A;Molecule type: DNA
A;Residues: 1-444 <KUR>
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C;Keywords: ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
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A;Accession: C71679
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DAND>
A;Rosidues: 1-495 <AND>
A;Rosidues: 1-495 <AND

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAWG-----DDEHLRKIEADV---PIY 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  272 IAISYLEKLDVINIKEALETFGGVKRRFNETTIANQ-VIVDDYAHHPREISATIETARK- 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 FEAAGLCPTVINGGIINNKSTNAYLG-----SSNYLIAEADESDATFIHIPSTIAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 YYGEKDSDD--IYAQNIQITDKGTAFDVYVD-----GEFYDHFLSPQYGDHTVLNALAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 TYGI-DSEDAHIIAFNINTDIASSTFDVKISLPNVLGTTIIEKITIPTPGRHNILNSLAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              330 -KYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 HFIGIGGVGMSGIARILHNIGYKVQGSDLVENY--NTKRLESYGIKIFLGQAKQNIKNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HFVGIKGSGMSSLAQIMHDLGHEVQGSD-IENYVFTEVALRNKGIKILPFDA-NNIKEDM
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 24.9%; Score 566; DB 2; Length 49
Best Local Similarity 33.3%; Pred. No. 3e-31;
Matches 158; Conservative 78; Mismatches 172; Indels
A; Reference number: A71630; MUID: 99039499; PMID: 9823893
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C; Species: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 30-Sep-2001
C; Accession: F97296
R; Nolling, U; Breton, G; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J; Bacteriol. 183, 4823-4838, 2001
A; Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc
A; Reference number: A96900; MUID:21359325; PMID:21359325
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UDP-n-acetylmuramate-alanine ligase (murC) RP247 - Rickettsia prowazekii
UDP-n-acetylmuramate-alanine ligase (murC) CFPccies: Rickettsia prowazekii
C,Species: Rickettsia prowazekii
C,Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C,Accession: C71679
C,Accession: C71679
R,Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE001437; PIDN:AAK81161.1; PID:g15026298; GSPDB:GN00168
A;Experimental source: Clostridium acetobutylicum AFCC824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175
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                                                                                                                                                                                                                                                                                                                               UDP-N-acetylmuramate-alanine ligase [imported] - Clostridium acetobutylicum
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                                                                420 IOKLONAY 427
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IQTYEYSF
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D.;
              Gispecies: Rickettesia conorii
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 22-Oct-2001
C;Accession: C97741
R;Ogata, H; Audic, S; Renesto-Audiffren, P; Fournier, P.E.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii. A;Reference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18;
                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-485 < CKUR>
A;Cross-references: GB:AE006914; PIDN:AAL02869.1; PID:g15619392; GSPDB:GN00173
A;Genetics:
A;Genetics:
A;Genetics: murC
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
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hypothetical protein murc [imported] - Rickettsia conorii (strain Malish 7)
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24.9%; Score 565.5; DB 2; Length
Best Local Similarity 33.5%; Pred. No. 3.2e-31;
Matches 161; Conservative 76; Mismatches 173; Indels
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A;Cross-references: GB:AE001180; GB:AE000783; NID:g2688755; PIDN:AAC67166.1; PID:g268876
A;Experimental source: strain B31
C;Superfamily: UDP-N-acetylmuramate-alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: H70201
R; Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White sor, C.M.; Casjens, S.; Hango, W.M.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, sownan, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A; Muthors: Smith, H.O.; Venter, J.C.
A; Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
A; Reference number: A70100; MUID:98065943; PMID:9403685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAH 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GKTSTT------GLLSHVMNGDKKTSFLIGDGTGM-GLPESDYFAFEACEYRRHFL 159
                                                                                                                                                                     335
                                                                                                                                                                                                                                                                                  DHMDTYGHSVEKLHQAFIDFIHRMPFYGKAFLCI-DSEHVRAILDKVSKPYATYGLDDTA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: H70201
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        UDP-N-acetylmuramate-alanine ligase (murC) homolog - Lyme disease spirochete
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REISATIETARKKYPHKEVVAVFOPHTFSRTOAFLNEFAESLSKADRVFLCEIFGSIREN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 FSLKQLDRSFDLIVYSSAYNKDGLQVLLEAKELNIPILSYPEALGELSRKYYSIGIAGSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 -ADVPIYYYGFKDSDDIYAQNIQITDKGTAFDVYVDGEFYDHFLSPQYGD-----HTVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 RKDISIFSYGSGDLSDFQISNIAVRSEYFCFS-----FLGLLNVELKTVLFHNVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-ALAVIAIS-YLEK--LDVINIKEAL----ETFGGVKRRFNETTIANQVI-VDDYAHHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 SYKPDYAIMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKG--IIAWGDDEHLRKIE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTNIKEALETFGGVKRRF---NETTIAN---QVIVDDYAHHPREISATIETARKKYPHKE
DHPD-YFKDINDVFDAFQEMAHNVK---KGIIAWGDDEHLRKI--EADVPIYYYGFKDSD
                                                                                 DIYAQNIQITDKGTAPDVYV-----DGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLD
                                                                                                            VVAVPOPHTFSRTGAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 468;
                                                                                                                                                                                                                                                                                                                                             -----EGASLINEDSINVLEQFDNAVILFMGAGDIQKLQNAYLD 429
                                                                                                                                                                                                                                                                                                                                                                   459 LEPIYCENVADL.PEMLLINVLQ--DGDIVLNWGAGSINRVPAALLE 501
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Best Local Similarity 31.0%; Pred. No. 2.3e-29;
Matches 148; Conservative 91; Mismatches 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-468 < KLE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-506 <PAR>
A;Cross-references: GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB85279.1; PID:g738068
A;Experimental source: serogroup A, strain 22491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SHVMN-GDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKYPHKE----WVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQD 385
                                                                                                                                         ----GLLSHVMNG----DKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIM 168
                                                                                                                                                                                -----SSNYLIAEADESDATFIHIPSTIAII 186
                                                                                                                                                                                                                                                                                                            220 YYGFKDSDD--IYAQNIQITDKGTAFDVYVD-----GEFYDHFLSPQYGDHTVLNALAV 271
                                                                                                                                                                                                                                                                                                                                         IAISYLEKLDVTNIKEALETFGGVKRRFNETTIA---NQVIVDDYAHHPREISATIETAR 328
                                                                                                                                                                                                                                                                                                                                                                                                                        LIDKIEGASLINEDSINVLEQFDNAV------ILFMGAGDIQKLQNAYLDKLGM 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HFIGIGGVGMSGIAEILYNLGYKVQGSDLVENY--NTKRLESYGIKIFLGHAEQNITNVS 74
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                                                                                                                                                                                                                                                     TNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAWG-----DDEHLRKIEADV---PIY
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                                                           VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTT-
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32.5%; Pred. No. 5.4e-30;
tive 79; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Gene: murC; NMA2061
C,Superfamily: UDP-N-acetylmuramate-alanine ligase
                                                                                                                                                                          Matches 151; Conservative
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R 477
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C; Keywords: ligase
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C,Superfamily:
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A,Experimental source: serogroup B, strain MC58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASILGAAGLDPTFVIGGKLNAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DHPD-YFKDINDVFDAFQEMAHNVK---KGIIAWGDDEHLRKI--EADVPIYYYGFKDSD 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DHMDTYGHSVEKLHQAFIDFIHRMPFYGKAFLCI-DSEHVRAILPKVSKPYATYGLDDTA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIYAQNIQITDKGTAFDVYV-----DGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLD 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DIYATDIENVGAQMKFTVHVQMKGHEQGSFEVVLNMP--GRHNVLNALAAIGVALEVGAS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
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419
                                 410 FNP-----DELSVKLFINIKKINKNTYFFKDVKDSINFIKSLLISGDLFITMGAGN 460
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   378 TGALTIQDLIDKIEGASLIN-
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C;Species. Caulobacter crescentus C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001 C;Accession: A87565 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,

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B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon I. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Accession: A87565
A;Accession: A87565
A;Status: preliminary
A;Molecule 'Ype: NNA
A;Residues: 1-473 < STO>
A;Cose-references: GB:AE005673; NID:g13424109; PIDN:AAK24517.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 HTESRIQAFLNEFAESLSKADRVFLCEIFGSIRENIGALTIQDLIDKIE-----GASLI 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 DHPDYFKDINDVFDAFQEMAHNVK-KGIIA-WGDDEHLRKIEADVP---IYYYGFKDSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 EHLDHWGDFDAVKKGFQDFIQNIPFYGFAAVCTDHPEVQALTSRIENRRLVTYGTNPQAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 IYAQNIQITDKGTAFDVYVD---GEF--YDHFLSPQYGDHTVLNALAVIAISYLEKLDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284 NIKEALETFGGVKRRFNETTIANOV-IVDDYAHHPREISATIETARKKYPHKEVVAVFQP
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                                                                                                                                                                                                                                                                                                                                Length 473;
                                                                                                                                                                                                                                                                                                                                                                        82; Mismatches 186; Indels
                                                                                                                                                                                                                                                                                                                         Query Match

23.5%; Score 534; DB 2;
Best Local Similarity 32.0%; Pred. No. 4.4e-29;
Matches 143; Conservative 82; Mismatches 186
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GenCore version 5.1.6
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OM protein - protein search, using sw model

June 3, 2004, 14:33:06; Search time 18 Seconds Run on:

{without alignments)
1264.148 Million cell updates/sec

Sequence:

US-10-712-713-2 2275 1 MTHYHFVGIKGSGMSSLAQI......GDIQKLQNAYLDKLGMKNAF 437 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 seqs, 52070155 residues Searched: Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description			staphyloc	baciling	bacilius		oceanopac		listeria			0								_				Q9jsz8 neisseria m				Q8e9p8 shewanella		9 agrobacter	ıo i	_	Q87wy6 pseudomonas
SUMMARIES		dī	MURC STAAM	MURC STAAU	MURC STAEP	MURC_BACAA		MURC BACSU		MURC_BACHD	MURC_LISIN	MURC LISMO	MURC_LACPL	MURC LACLA	MURC STRP3	MURC STRPY	MURC STRP8	MURC STRR6	MURC_STRPN	MURC THETN	MURC CLOAB	MURC CLOPE	MURC_FUSIN	MURC_RICPR	MURC RICCN	MURC_NEIMA	MURC_BORBU	MURC NEIMB	MURC CAUCR	MURC_SHEON			- 1		MURC_PSESM
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Q8ym75 anabaena sp Q92nm0 rhizobium m Q7vmy1 haemophilus Q9p1g1 c murc/dd1 Q8d2z7 wiggleswort Q8yi65 brucella me Q8div5 synechococc P59418 buchnera ap Q8x9y7 escherichia P17952 escherichia Q8x99t salmonella Q8z9g8 salmonella
MURC_ANASP MURC_RHIMB MURC_HAEDU MUDD_CHIMU MURC_BRUME MURC_SYNEL MURC_BUCBP MURC_ECOL6 MURC_ECOL1 MURC_ECOL1 MURC_ECOL1
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## ALIGNMENTS

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Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1282;
-!- SIMILARITY: Belongs to the murCDEF family.
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                                                                                                                                                                                                                                                                                                                                                                                               Length 437;
                                    PIR; H89958; H89958.
HAMAP; MF 00046; -; 1.
InterPro; IPR000111; Mur_ligase.
InterPro; IPR005758; Mur_l.
Ffam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase; 1.
IGRPAMS; TIGRL082; murc; 1.
Ilgase; ATP-binding; Cell division; Cell wall; Ingase; ATP-binding; Cell division; Cell wall; NP_BIND 109 114 ATP (POTENTIAL).
SEQUENCE 437 AA, 49174 MW; 3349943079D87355 CRC64;
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (BC 6.3.2.8)
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                            ; Score 2274; DB 1;
Pred. No. 1.7e-142;
1; Mismatches 0;
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Best Local Similarity 99.8
Matches 436; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 437;
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR004578; Mur_ligase; 1.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase; 2.
IIGRFAMs; IIGR01082; murC; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding.
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437 AA, 49176 MW, E2FC7D79E6CF8361 CRC64;
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
acetylmuramoyl-L-alanine synthetase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 2255; DB 1; 98.9%; Pred. No. 2.9e-141;
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acetylmuramoyl-L-alanine synthetase)
                                                                                                                                                                                                                                                                                                                                           Nature 423:81-86(2003).
-!- FUNCTION: Cell wall formation.
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Best Local Similarity
                                                                                                              MURC OR BA4938.
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                                                                                                                                                                                                                                                                                                           Framer C.M.;
                               MURC BACAA
                                          281KQ2;
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                                                                                                                                                                                                                                                                                                                                                                                                    437 AA; 49578 MW; 2DB8BFD5D9C1C334 CRC64;
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HAMAD; MF 00046; -; 1.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005768; MurC.
Pfam; PF02875; Mur_ligase_C; 1.
Ffam; PF02875; Mur_ligase_C; 1.
Ilgase, ATP-binding; Cell division; Cell wall; Peptidoglycan synthesis; Complete proteome.
NP_BIND 108 HAPP (POTENTIAL).
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SEQUENCE FROM N.A.
STRAIN=ATCC 12228;
PubMed=12950922;
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-i- PATHWAY: Peptidoglycan biosynthesis.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- SUBCELLULAR: Belongs to the murCDEF family.
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InterPro; IPR004101; Mur_ligase.
InterPro; IPR004101; Mur_ligase.
InterPro; IPR004101; Mur_ligase.
InterPro; IPR004578; Murc.
InterPro; IPR01085; Murc.
InterPro; IPR01082; Murc.
Ingase; ATP-binding; Cell division; Cell wall;
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                                                                                                                                                                                                                                                                                                               Bacillus anthracis (strain Ames).
Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=198094;
10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
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64.7%; Pred. No. 1.3e-89;
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70C37FCFBCFFAE74 CRC64;
Peptidoglycan synthesis; Complete proteome. NP BIND 108 114 ATP (POTENTIAL)
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                                                                                                                                                            TAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
                                                                                                                                                                                                                                                                                      MEDILINE-22008415; PubMed=12721630;
Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B.,
Raparal V., Bhattacharyya A., Reznik G., Mikhailova N., Lapidus A.,
Gutu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T.,
Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D.,
Overbeek R., Kyrpides N.;
Genome sequence of Bacillus cereus and comparative analysis with
Bacillus anthracis.";
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-!- FUNCTION: Cell wall formation.
-!- FUNCATION: Cell wall formation.
-!- CATIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine
phosphate + UDP-N-acetylmuramoyl-L-alanine.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
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Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
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InterPro; IPR000713; Mur ligase.
InterPro; IPR004101; Mur ligase_C.
InterPro; IPR005758; MurC.
Pfam; PF01225; Mur ligase; 1.
Pfam; PF02875; Mur ligase; 2.
IGR01082; murC; 1.
Ligase; ATP-binding; Cell division; Cell wall;
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SEQUENCE FROM N.A.
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                                                                                                                                                                 1 MIVYHFVGIKGTGMSSLAQILHDMKHTVQGSDYEKRFFTQTALEKRSISILPFDKNNVEE
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Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
"Sequencing and functional annotation of the Bacillus subtilis genes
in the 200 kb rrnB-dnaB region.";
Microbiology 143:3431-3441(1997).
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                                                             ;
Query Match 64.6%; Score 1470; DB 1; Length 436; Best Local Similarity 64.7%; Pred. No. 1.3e-89; Matches 279; Conservative 58; Mismatches 94; Indels (
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15-JUL-1998 (Rel. 36, Last sequence update)
16-JUL-1998 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-acetylmuramoyl-L-alanine synthetase).
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
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RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N., RA Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M., Klein C., Kobayashi Y., Koetter P., Kohingstein G., Krogh S., Kumano M., Lavine A., Liu H., Masuda S., Mauler J., Lazarevic V., Lee S.M., Lavine A., Liu H., Masuda S., Mauel C., Medigue C., Medina M., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., RA Porno D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Presecan E., Pujic P., Purnelle B., Rappoort G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y., Sacorin E., Schulan E., Schleeter R., Scoffone F., Sator T., Scanlan E., Schleeter R., Scoffone F., RA Seriguchi J., Sekoweka A., Serox S.J., Serror P., Shin B.S., Soldo B., Raeuchi M., Tamakoshi A., Tanaka T., Tarahashi H., Takemaru K., Yananakoshi A., Tanaka T., Terpetra P., Nambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A., Tarahills.", Sephills."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Varon D., Brody M.S., Price C.W.; "Bacillus subtilis operon under the dual control of the general stress transcription factor sigma B and the sporulation transcription factor sigma H.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP
phosphate + UDP-N-acetylmuramoyl-1.-alanine.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
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Subtilist; BG10973; murc.
Subtilist; BG10973; murc.
Interpro; IPR004101; Mur ligase.
Interpro; IPR004101; Mur ligase.
Interpro; IPR005758; Murc.
Interpro; IPR01225; Mur ligase.
Interpro; IPR01225; Mur ligase.
Interpro; IPR01825; Mur ligase.
Interpro; IPR01825; Mur ligase.
Interpro; IPR01982; murc.
IPR01988; IPR01988; IPR01988; Cell wall; Cell division; Ligase;
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432 AA; 48364 MW; B73BF9502FD7CEIB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 390:249-256(1997).
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61 DMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS 120
                                                                121 HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFK 180
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                                                                                 TAFDVYVDGERYDHFLSPQYGDHTVIMALAVIAISYLEKLDVTNIKEALETFGGVKRRFN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 30:3927-3935 (2002).

-i - FUNCTION: Cell wall formation.

-i - CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP phosphate + UDP-N-acetylmuramoyl-L-alanine.

-i - PATHWAY: Peptidoglycan blosynthesis.

-i - SUNCELLULAR LOCATION: Cytoplasmic (Probable).

-i - SUNLIARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=HTB831 / DSM 14371 / JCM 11309;
MEDLINE=22220767; PubMed=12235376;
Takami H., Takaki Y., UChiyama I.;
"Genome sequence of Oceanobacillus iheyensis isolated from the Iheya Ridge and its unexpected adaptive capabilities to extreme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_
InterPro; IPR005759; MurC.
Pfam; PF01225; Mur_ligase_1:
Pfam; PF012875; Mur_ligase_C; 1.
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DB 1; Length 432;

63.2%; Score 1438; DB 1; Length 43 64.6%; Pred. No. 1.6e-87; ive 51; Mismatches 100; Indels

Query Match
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1 MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKE

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NCBL_TaxID=1642;
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
                                                                                                                                                                                                                                                  Query Match 60.1%; Score 1368; DB 1;
Best Local Similarity 59.3%; Pred. No. 6.6e-83;
Matches 253; Conservative 69; Mismatches 105;
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MEDLINE=20512582; PubMed=11058132;
Arkami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                       7
                                                                                                                                                                   DB 1; Length 438;
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10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                   ; Score 1381.5; DB 1; Length; Pred. No. 8.7e-84; 63; Mismatches 102; Indels
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                                                                                                                     43AE610786AB1992 CRC64;
          TIGRFAMS; TIGRO1082; murC; 1.
Ligase; ATP-binding; Cell division; Cell wall;
Peptidoglycan synthesis; Complete proteome.
ATP (POTENTIAL).
SEQUENCE 438 AA, 49863 MW, 43AE610786AB199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           433 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                      60.7%;
61.1%;
                                                                                                                                                                Query Match
Best Local Similarity 61.1%
Matches 261; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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SEOUENCE FROM N.A.
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Q9K7W1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 ]
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                               361 LADBÝYLCDÍPGSARBKTGNLTIADLAHKTKGNHIÍKEBHTEBLLQYPBAVILFMGAGDV 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-EGD-e / Serovar 1/2a;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

MEDLINE=21537279; PubMed=11679669;

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,

Entian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Brian K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,

Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,

Johnsons L.-M., Kaerst U., Kreft J., Kihh M., Kunst F., Kunspkat G.,

Madueno B., Maitournam A., Mata Vicente J., Ng E., Nodjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlubeter T., Simose N., Tierrez A.,

Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;

"Comparative genomics of Listeria species.";

Comparative Pertidoglycan biosynthesis.

Comparative Pertidoglycan biosynthesis.

Comparative Section Signal Boognythesis.

Comparative Section Signal Boognythesis.

Comparative Section Signal Boognythesis.

Comparative Section Signal Boognythesis.

Comparative Section Signal Boognythesis.
       361 KADRVFLCEIFGSIRENTGALTIQDLIDKIBGASLINEDSINVLEQFDNAVILFMGAGDI
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
10-PCN-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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59.7%; Pred. No. 3.6e-81;
tive 64; Mismatches 108;
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InterPro; PR004013; Mur_ligase.
InterPro; PR004101; Mur_ligase_C.
InterPro; PR004518; Mur_ligase_C.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
IIGRAMs; TIGRO1082; murCf_1.
IIGRAMs; ATP-binding; Cell division; Cell wall;
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Peptidoglycan synthesis; Tomplete proteome.
NP BIND 108 114 ATP (POTENTIAL)
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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Best Local Similarity
                                                                                                                                                    OKLONAY 427
                                                                                                                                                                                                                       421 OKFOAAY 427
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MURC LISMO
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STRAIN=CLIP 11262 / Serovar 6a;

X Glaser Promine A. Buchrieser C., Rusnick C., Amend A.,

A Glaser P., Frangeul L., Buchrieser B., Chakraborty T.,

Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,

A Gharbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,

A Domann E., Dominguez-Bernal G., Duchaud B., Durant L., Dussurget O.,

Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,

A Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,

A Madueno E., Maitournam A., Mata Vicente J., NG E., Nedjari H.,

Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

A Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

Science 294:849-852 (2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: AIP + UDP-N'acetylmuramoyl + L-alanine = ADP
-!- Dhosphate + UDP-N'acetylmuramoyl-L-alanine.
-!- PATHWAY: Peptidoglycan biosynthesis.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the murCDEF family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   447 AA; 50036 MW; AFA793A96833E904 CRC64;
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PIR; AE1638; AE1638
ListLinist; LINO1646; -.
HAMAP, MF 00046; -; 1.
InterPro; IPR0040713; Mur_ligase.
InterPro; IPR004011; Mur_ligase.
InterPro; IPR005758; Mur_ligase.
Pfam; PF01225; Mur_ligase, 1.
Pfam; PF01255; Mur_ligase, 2.
ITGRFAMS; ITGR01082; Mur_ligase, 2.
InterPro; IPR001082; Mur_ligase, 3.
InterPro; IPR001082; Mur_ligase, 3.
InterPro; IPR01082; Mur_ligase, 3.
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NP BIND 108 114 ATP (POTENTIAL)
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Best Local Similarity 60.21
Matches 257; Conservative
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                                                                                                                                                                                             2 THYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKED
                                                                                                                                                                                                            182 INDVFDAFQEMAHNVKKGITAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGT
                                                                                                                                                                                                                                                                                                                                                                                                     242 AFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKBALETFGGVKRRFNE
                                                                                                                                                                                                                                                                                                                                                                                                                  245 SFEVKYHDESLGKFEIPLFGEHNVINSTAVIAVSYFEKVNLDEIRRELLDFSGVKRRFSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 MVVIQGNAFASSHEBIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH
                                                                                                                                                                                                                                                               VANGDXKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKD
                                                                                                                                                                                                                                                                                                                                                                             185 LADVOSAPOOFGNOVKKGIFAWGDDESLRHLDVDTPIYYYGTNDRDDFQAVNIKRTTKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 ADRVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                       1;
                                                                                                                                                DB 1; Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
BERBA-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                56.5%; Score 1284.5; DB 1; Length
55.7%; Pred. No. 2.1e-77;
ive 75; Mismatches 115; Indels
                                                                                                                        25A582D850238CD4 CRC64;
      EMBL; AL935256; CAD63921.1; -.
HAMAP; MF 00046; -; 1.
InterPro; IPR000713; Mur ligase.
InterPro; IPR004011; Mur ligase.C.
Pfam; PF01225; Mur ligase; 1.
Pfam; PF02875; Mur ligase C; 1.
Iigase, ATP-binding; Cell division; Cell wall; Peptidoglycan synthesis; Complete proteome. NP BIND 111 117 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acetylmuramoyl-L-alanine synthetase)
MURC OR LL2040.
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MEDLINE=21235186; PubMed=11337471;
                                                                                                                        436 AA; 48750 MW;
                                                                                                                                              Query Match
Best Local Similarity 55.7%;
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 QKLQNAYLDKL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKYEKIYEDOM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
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16-OCT-2001 (
28-FEB-2003 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SSI-1 / Serotype M3;
MEDLINE=22683278; PubMed=12799345;
Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
Hayashi H., Hattori M., Handada S.,
"Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
"large-scale genomic rearrangement in invasive strains and new insights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 13:1042-1055(2003).

-1- FUNCTION: Cell wall formation.

-1- CATALYTIC ACTIVIT: ATP + UDP-N-acetylmuramcyl + L-alanine = ADP-DROSPHARE + UDP-N-acetylmuramcyl-L-alanine.

-1- PATHWAY: Peptidoglycan blosynthesis.

-1- SUBCELLULAR LOCATION: Oytoplasmic (Probable).

-1- SUBCRILULAR LOCATION: Oytoplasmic (Probable).

-1- SIMILARITY: Belongs to the murcDEF family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Gaps
                                                                                                                                                                                            MEDLINE=22133808; PubMed=12122206;
Beres S.B., Sylva G.L., Barbian K.D., Lei B., Hoff J.S.,
Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
Schlievert P.M., Musser J.M.;
"Genome sequence of a serotype M3 strain of group A Streptococcus:
phage-encoded toxins, the high-virulence phenotype, and clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 442;
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Matches 218; Conservative 82; Mismatches 128; Indels
Streptococcus pyogenes (serotype M3).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C0216CAEFE922A03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptidoglycan synthesis; Complete proteome.
NP BIND 109 115 ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MP_00046; -; 1
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005758; MurC.
Pfam; PF0125; Mur_ligase; 1.
Pfam; PF02255; Mur_ligase; 1.
TIGRFAMS; TIGR01082; murC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 AA; 49622 MW;
                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=MGAS315 / Serotype M3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        into phage evolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                     NCBI_TaxID=198466
                                                                                                                                                                                                                                                                                                                                                                                                         emergence."
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 FDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNET
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52.7%; Pred. No. 1.6e-70;
ive 79; Mismatches 121; IndelB
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28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
MURC OR SPYM3_0252 OR SPS1607.
                                   PATHWAY: Peptidoglycan biosynthesis.
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the murCDEF family.
                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006433; AAK06138.1; ALT_INIT.
HAMAP; MF_00046; -; 1.
InterPro; IPR000413; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005758; Mur_ligase_C.
Pfam; PF02255; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase; 2; 1.
IIGREAMS; TIGR01082; MurC; 1.
Ingase; ATP-binding; Cell division; Cell wall;
           phosphate + UDP-N-acetylmuramoyl-L-alanine
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Best Local Similarity 52.7%
Matches 227; Conservative
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| OKYELAF-EKL 434
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Q8K8J5;
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                                                                                                                 304 IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKAD 363
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                                                 244 DVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALETFGGVKRRFNETT 303
                                                                      245 KVKHQGEVIGQEHVPAYGKHNILNATAVIANLEVAGIDMALVADHLKTFSGVKRRFTEKI 304
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Perretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Oian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J.,
Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663 (2001).
-!-FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP +
                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
UD-OCT-2003 (Rel. 42, Last annotation update)
UDP-N-acetylmuramate--1-alanine ligase (EC 6.3.2.8) (UDP-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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--- PATHWAY: Peptidoglycan blosynthemia.
--- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
--- SIMILARITY: Belongs to the murCDEF family.
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                                                                                                                                                                                                                                                                                                                                                                      442 AA
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STRAIN=SF370 / ATCC 700294 / Serotype M1;
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR0007101; Mur_ligase_C.
InterPro; IPR005758; Murc.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
TIGRFAMB; TIGR01082; murc; 1.
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STRAIN=MGAS8232 / Serctype M18;
MEDLINE=21927593; PubMed=11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Syva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Rapur V., Daly J.A., Veasy L.G., Musser J.M.,
"Genome sequence and comparative microarray analysis of serctype M18
group A Streptococcus strains associated with acute rheumatic fever outbreaks."
                                             4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
                                                                   64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM
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-!- FUNCTION: Cell wall formation.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl + L-alanine = ADP
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50.7%; Pred. No. 7.9e-68; ive 82; Mismatches 128; Indels
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Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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-L-alanine ligase (EC 6.3.2.8)
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--- PATHWAY: Peptidoglycan biosynthemia.
--- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
--- SUBLARITY: Belongs to the murCDEF family.
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InterPro; IRR000713; Mur_ligase.

InterPro; IRR000713; Mur_ligase.

InterPro; IRR000713; Mur_ligase.

Ffam; PF01225; Mur_ligase; 1.

Pfam; PF01225; Mur_ligase; 1.

IGRFAMS; TIGARD1082; MurC; 1.

Ingase; ATP-binding; Cell division; Cell wall;

Peptidoglycan synthesis; Complete proteome.

NP BIND 109 1115

SEQUENCE 442 AA; 49583 MW; 52535CCDDA3356E7 CRC64;
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Query Match
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Search completed: June 3, 2004, 14:39:38 Job time : 19 secs

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Q8dy77 streptococc
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Q8dsp4 streptococc
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Q899j1 clostridium
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	Q894q4 bilidobacte Q82107 atreptomyce Q89fu8 bradyrhizob Q821s4 chlamydophi	_			Q7vqi7 candidatus Q8de91 vibrio vuln Q8ph24 xanthomonas		
Q7VEJ1 Q7VMY1 Q9RGR6 Q83MF8 Q88N75	Q8G4Q4 Q82L07 Q89FU8 Q821S4	Q9KGV8 Q8A259 Q7V9C3	Q7UA71 Q8KCE3 Q9CMA5	Q7VJ70 Q7VN73 Q8XVP8	27VQ17 28DE91 28PH24	087576 083GN1 0874J0 083HK2	Q87SV8 Q9JUE5 Q9JRY9 Q8EYR2
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472 475 487 491	512 464 467 811	190 467 488	467 474 457	439 459 461	488 484 452	452 475 490 75	4 4 4 4 5 2 2 4 4 5 5 8 4 5 8 8 5 8 8 5 8 5 5 5 5 5 5
21.9 21.9 21.5 21.5 21.5	21.3 20.9 20.9	20.3	19.9 19.7 19.3	18.7 18.6 18.5	18.1 17.8 17.5	17.1 17.3 17.3	
498.5 498.5 490 490 488.5	484.5 480 474.5 464	462.5 462 456	452.5 449 439.5	426 424 420.5	412.5 405 399	398 393.5	
11 118 119 21	2 2 2 2 2 2 2 3 3 3 4 7	25 24 28 28	30 30 310	6 8 6 6 8 6	35 36 37	8 8 8 4 4 8 6 0 1	1 4 4 4 4 1 5 6 4 5

## **ALIGNMENTS**

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SEQUENCE FROM N.A.

STRAIN-V583 / ATCC 700802;

MEDLINE-22550857; PubMed=12663927;

MEDLINE-22550857; PubMed=12663927;

MEDLINE-22550857; PubMed=12663927;

Read T.D., Fouts D.E., Bisen J.A., Gill S.R., Heidelberg J.F.,

Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,

Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,

Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,

Utterback T., Radune D., Kerchum K.A., Dougherty B.A., Fraser C.M.;

"Role of mobile DNA in the evolution of vancomycin-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CO: GO:0005737; C:cytoplasm; IEA.

GO: GO:0005524; F:ATP binding; IEA.

GO: GO:0016674; F:ligase activity; IEA.

GO: GO:0009058; F:Ilgase activity; IEA.

GO: GO:0009058; P:biosynthesis; IEA.

GO: GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
                                                                                                                                                          Enterococcus faecalis (Streptococcus faecalis).
Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
NCBI_TaxID=1351;
                                                                    (TrEMBLrel. 24, Created)
(TrEMBLrel. 24, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
                                   445 AA.
                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Last and UDP-N-acetylmuramate-alanine ligase MURC OR EF1908.
                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005758; Murc.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
TIGRFAMS; TIGR01082; murC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 299:2071-2074(2003).
EMBL; AE016953; AAO81660.1; -.
TIGR; EF1908; -.
                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus faecalis.
                                                                        01-JUN-2003
                                                                                           01-JUN-2003
                                                     Q833N6;
                                     9833N6
RESULT 1
                    0833N6
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25A582D850238CD4 CRC64;
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GO; GO:0005840; C:ribosome; IEA.
GO; GO:0005524; F:ATP binding; IEA
Ligase; Complete proteome.
SEQUENCE 436 AA; 48750 MW;
                                                                                       Best_Local Similarity 55.7%
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 OKLONAYLDKL 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 QKYEKIYEDQM 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                 Query Match
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A Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
A Kleerebezem M., Boekhorst J., van Kranenburg R., Sandbrink H.M.,
A Fiers M.W.E.J., Stekema W., Klein Lankhorst R.M., Bron P.A.,
A Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
De Vos W.M., Slezen R.J.;
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
"Complete genome sequence of Lactobacillus plantarum WCFS1.";
Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
R. BMBL; AL935Z6; CAb63921.1;
GO; GO:0005524; F:ATP binding; IEA.
R. GO; GO:000568; F:Ligase activity; IEA.
R. GO; GO:0009058; F:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.
R. InterPro; IPR004101; Mur. ligase.
R. InterPro; IPR004101; Mur. ligase.
R. Refem; PF01225; Mur ligase.
R. Pfam; PF01255; Mur ligase.
R. Refem; PF0225; Mur ligase.
R. Refem; PF0225; Mur ligase.
R. Refem; PF0225; Mur ligase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 VIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHVM 123
                                                                                                                                                                                                                                                                                                                                                        124 NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN 183
                                                                                                                                                              63
                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                   309 VSDMIIVDDYAHHPAEIKATIDGARQKYPDKEIIAVFQPHTFTRTIALMDEFAEALDLAD
                                                                                                                                                              4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 IANOVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVFLCEIFGSIRENTGALTIODLIDKIE-GASLINEDSINVLEQFDNAVILFMGAGDIOK
                                                                                                                                                                                         Gaps
                                                                                                                  1;
                                                                    DB 16; Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactobacillus plantarum.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                86; Indels
                        445 AA; 49999 MW; 12189004F4FBIE9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate--alamin ligase (EC 6.3.2.8).
                                                                 63.2%; Score 1438.5; DB : 60.9%; Pred. No. 1.2e-92; iive 79; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 AA
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STRAIN=NCIMB 8826 / WCFS1;
    Ligase; Complete proteome
                                                                                                                     Matches 259; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                      Query Match
Best Local Similarity
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                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 SFEVKYHDESLGKFEIPLFGEHNVLNSTAVIAVSYFEKVNLDEIRRELLDFSGVKRRFSE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 TTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSK 361
                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 INDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 ADRVFLCEIFGSIRENTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDI
                                                                                                                                              62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLISH
                                                                                                                                                                                                                                                                                                                                                  122 VMNGDXXTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKD
                                                                                                                2 THYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKED
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                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence and comparative genomic analysis of ar emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
DB 16; Length 436;
                                                           1,
56.5%; Score 1284.5; DB 16; Lengt
55.7%; Pred. No. 7.6e-82;
ive 75; Mismatches 115; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agalactiae (serotype V).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae;
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Last sequence update)
Last annotation update)
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01-WAR-2003 (TrEMBLrel. 23, Last Bequ
01-WAR-2003 (TrEMBLrel. 23, Last enc
01-0CT-2003 (TrEMBLrel. 25, Last anno
UDP-N-acetylmuramate--alanine ligase.
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STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
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245 FKVFYNQEBIGQFHVPAYGKHNILMATAVIANLYIMGIDMALVABHLKTFSGVKRRFTEK 304
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GO:000524; F:ATP binding; IEA.
GO:000524; F:ATP binding; IEA.
GO:000574; F:Ingase activity; IEA.
GO:000573; F:Etructural constituent of ribosome; IEA.
GO:0008763; F:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.
GO:0009058; P:biosynthesis; IEA.
GO:0009273; P:cell wall blosynthesis (sensu Bacteria); IEA.
GO:0006412; P:protein biosynthesis; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 YHPIGIKGSGMSALALMLHQMGHNVQGSDVDKYYFTQRGLBQAGVTILPFSPNNISEDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 NDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITDKGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALBIFGGVKRRFNET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 VIQGNAF-ASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 TIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKA
                         Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.7%; Score 1153.5; DB 16; Length 443; Best Local Similarity 51.0%; Pred. No. 1.2e-72; Matches 220; Conservative 82; Mismatches 126; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLOMAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 25, Last annotation update)
Putative UDP-Nacetyl muramate-alanine ligase (EC 6.3.2.8)
MURC OR SMU.1731.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                                                                                                                                                                         InterPro; IPR005798; Murc.
InterPro; IPR000713; Murligase.
InterPro; IPR004101; Murligase.
InterPro; IPR001706; Ribosomal_L35.
Pfam; PF01225; Murligase, 1.
Pfam; PF02875; Murligase. C; 1.
TIGRPAMS; TGR01085; Murc.
IPROSTIE; PS00936; RIBOSOWAL_L35; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 443 AA; 49836 MW; OBDBD0CDBC6.
                                           invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002)
EMBL; AL766852; CAD47323.1; -.
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QLYERSFEELL 435
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Q8DSP4;
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RGO; GO:0016974; F:ligase activity; IEA.

GO; GO:003735; F:structural constituent of ribosome; IEA.

GO; GO:0009735; F:structural constituent of ribosome; IEA.

RGO; GO:0009058; P:biosynthesis; IEA.

GO; GO:0009273; P:cell wall biosynthesis; (sensu Bacteria); IEA.

RO; GO:0006412; P:procein biosynthesis; IEA.

RILEPPO; IPRO0575; Mur. ligase.

RILEPPO; IPRO0713; Mur. ligase.

RILEPPO; IPRO0713; Mur. ligase.

RILEPPO; RE01006; Ribosomal_E35.

RETERPO; RE01006; Ribosomal_E35.

RETERPOS; RE010082; Mur. ligase.

RETERPOS; RE010082; Mur. ligase.

REGNAMS; TIGRO1082; Mur. ligase.

REGNAMS; REGNAMS LISSS MA; CIDEFCTDEG017228 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 NGSDFKVFYNQEEIGQFHVPAYGKHNILNATAVIANLYIMGIDMALVABHLKTFSGVKRR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FNETTIANOVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAES 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              359 LSKADRVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKDINDVFDAFQEMAHNVKKGIIAWGDDEHLRKIEADVPIYYYGFKDSDDIYAQNIQITD 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMV
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MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Bubhrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Gaps
                                                                                                                                                                                                                                                                                                                                                                                    Length 443;
                                                                                                                                                                                                                                                                                                                                                                                  51.1%; Score 1163.5; DB 16; Lengt
51.3%; Pred. No. 2.4e-73;
iive 81; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae (serotype III).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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AGDIQLYERSFEELL 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 223; Conservative
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MURC OR GBS1664.
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Best Local
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123 -MNGDKKTSFLIGD-----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNID 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    288 ALETFGGVKRRFNETTIANQV-IVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTFS 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 RTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKI--EGASLIN----EDS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              307 GLESFHGTHRRFELKGVRNDVIVIEDYAHHPTEIKATL-SAAKNYPSNRILCVFQPHTYT 365
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Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).

EMBL; ARD15936; ARO34355.1;

GO; GO:0005224; F:ATP binding; IEA.

GO; GO:0006763; F:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.

GO; GO:0009763; F:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.

GO; GO:0009763; P:UDP-N-acetylmuramate-L-alanine ligase activity; IEA.

InterPro; IPR000713; Mur ligase.

InterPro; IPR004101; Mur ligase.

Pfam; PF02875; Mur ligase.

Pfam; PF02875; Mur ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 HFIGIGGISMSGMAEILLKKGYKVSGSDSTKSPIID-KLINLGAEIYIGHKAENIKNVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VIQCNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYT-SVAVTGAHGKTSTTGLLSHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 ADHLDYYKDINHIKNAFSKFANLIPKDGYLIACAEDENINDIIKNIDCTIITYGL-NKGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229 IYAQNIQITDKGTA-FDVYVDGEFYDHFLSPQYGDHTVINALAVIAISYLEKLDVTNIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKEDMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 FDHPDYFKDINDVFDAPQEMAHNVKKG--IIAWGDDEHLRKI--EADVPIYYYGFKDSDD
                                                                                                                          Clostridium tetani.
Bacteria, Firmicutes, Clostridia, Clostridiales, Clostridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                            "The genome sequence of Clostridium tetani, the causative agent
                                                                                                                                                                                                                                                                                                                                     Brueggemann H., Baeumer S., Frické W.F., Wiezer A., Liesegang
Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
Gottschalk G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
27.8%; Score 633.5; DB 16; Length
Best Local Similarity 35.1%; Pred. No. 3.8e-36;
Matches 158; Conservative 91; Mismatches 168; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456 AA; 50816 MW; 31C71A197188CBB5 CRC64;
                01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8).
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01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                            STRAIN=Massachusetts / E88;
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SEOUENCE 456 AA; 50816
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                                                                                                                                                                                                              NCBI_TaxID=1513;
                   01-JUN-2003
01-OCT-2003
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Q9RNM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDHPDYFKDIN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 RVFLCEIFGSIRE-NTGALTIQDLIDKI-EGASLINEDSINVLEQFDNAVILFMGAGDIQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                         Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Qian Y., Lin S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti J.J.; "Genome sequence of Streptococcus mutans UAL59, a cariogenic dental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KNITDTSYLIGDGGRGLANSQYFVFESDEYERHFMPYHPEYSIITNIDFDHPDYFIGVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFOPHTFSRTQAFLNEFAESLSKAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKILPFDANNIKEDMVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49.8%; Score 1132.5; DB 16; Length 452; 50.7%; Pred. No. 3.7e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50903 MW; 4AD29B2CCA6576CE CRC64;
                                                                                                                                                                                                                                                                     pathogen.";
Proc. Nat1. Acad. Sci. U.S.A. 99:14434-14439(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 AA.
                                                                                                       ATCC 700610 / Serotype C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                  MEDLINE=22295063; PubMed=12397186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
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Best Local Similarity
                           NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     218;
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SEQUENCE
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122 V-MNGDKKTSFLIGD----GTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNIDFDH 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 ALNFVQQGYSSHFTLRRDGVEDIAVMYNLPGEHNVLNALASIAVATEDEIEDEAIVLALA 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |||: ::| |||: |: | : | :: | : | 393 SRIRDLYDDFVEVLSQVDCLILLDVYSAGEAPVPGADSRALCRSIRQ------RGQLDP 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 MVVIQGNAFASSHEEIVRAHQIKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AQNIQITDKGTAFDVYVDGEFYDHFLSPQYGDHTVLNALAVIAISYLEKLDVTNIKEALE 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 TFGGVKRRFNE----TTIANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTF 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SRIQAFLNEFAESLSKADRVFLCEIFG------SIRENTGALTIQDLIDK 389
                                                                                                                                                                                                                Ishii A., Nakasone K., Sato T., Sugai M., Wachi M., Nagai K., Kato C., "Isolation and characterization of dcw gene cluster for cell division and cell wall synthesis from a deep-sea piezophilic Shewanella violacea.";
                                                                                                                                                                                                                                                                                                            Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB052554; BAB19203.1; -.

GO; GO:000573; C:cytoplasm; IEA.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:000876; F:biosynthasmate-L-alanine ligase activity; IEA.

GO; GO:0009058; P:biosynthasis; IEA.

GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 PD-YFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADV--PIYYYGFKDSDDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKED
                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01225; Mur_ligase; l. —
Pfam; PF02875; Mur_ligase C; l.
TIGREAMS; TIGR01082; m.urC; m. 96E45B6A503E48E2 CRC64;
SEQUENCE 494 AA; 54098 MW; 96E45B6A503E48E2 CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Murc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%; Score 523.5; DB 2; 31.8%; Pred. No. 2.2e-28; iive 88; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 IEGASLINEDSINVLEOF--DNAVILFMGAGDIOKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR005758; MurC.
InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 31.8%;
Matches 145; Conservative 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 LDAGGIDPTVINGGIINSY----GSNARLGDSDWWVVEADESDGSFLRLDGTLAIVINID 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 VVVVSSAIHRGNDEVEAALENRIPVVRRAEMLAELMRLKSTVAVAGTHGKTTTTSMVAAL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 ADIRAVDITPISGGNRFTAVIRGRDGDIRRIENIFLPMPGRHNIQNALSAIGVALEFSIP 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 DAAIRDGFARFGGVKRRFSRVGIKICDGSVLVIDDYGHHPVEIKAVLSAARES-AQORV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 VAVFQPHTFSRTQAFLNEPAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG---- 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 IÁVVÓPHRFLRLHDLMTEFQSAFNDÁDMVFVAPVYAAGEQPIAGVDSÓALVSGLKQHGHR 423
                                                                                                                                                                                                                                                                                         "Sequence analysis of 41E10 fosmid clone of Zymomonas mobilis.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; API79611; ADDSJ355.1;
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; F:ATP binding; IEA.
GO; GO:000874; F:ligase activity; IEA.
GO; GO:0008763; F:blosynthesis; IEA.
GO; GO:000973; P:cell wall biosynthesis (sensu Bacteria); IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 HFVGIGGIGMSGIAEVMHNLGYQVQGSDISEGY--TVDALRQMGIKVLIGHHAENVKDAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----HVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMTNID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 FDHPDYFKDINDVFDAFQEMAHNVKKGIIAWGDDEH-----LRKIEADVPIYYYGFKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              227 DDIYAQNIQITDKGTAFDVYV---DGEF--YDHFLSPQYGDHTVLNALAVIAISYLEKLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 VTNIKEALETFGGVKRRFN---ETTI--ANQVIVDDYAHHPREISATIETARKKYPHKEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDI-ENYVFTEVALRNKGIKIL-PFDANNIKEDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gape
                                                                                                                                    Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.6%; Score 536.5; DB 2; Length 486; 32.5%; Pred. No. 2.7e-29; ative 75; Mismatches 174; Indels 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ASLINEDSINVLEOFDNAVILFMGAGDIOK 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       424 SAQAVDSPRSLAIALADIİKADDİ------İICVGAĞDİTK 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    486 AA; 52602 MW; 7DB255E70F47CCD4 CRC64;
                  01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate-alanine ligase.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005758; Murc.
InterPro; IPR000713; Mur ligase.
InterPro; IPR004011; Mur ligase.C.
Pfam; PP01225; Mur ligase; 1.
Pfam; PF02875; Mur ligase.C. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGREAMS; TIGR01082; murc; 1.
                                                                                                                                                            Sphingomonadaceae; Zymomonas
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Matches 151; Conservative
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                                                                                                                                                                                                                                               STRAIN=ZM4;
Um H.W., Kang H.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                               Zymomonas mobilis.
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                 NCBI_TaxID=542;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HFVGIKGSGMSSLAQIMHDLGHEVQGSDI-ENYVFTEVALRNKGIKI-LPFDANNIKEDM 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-YFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADVP--IYYYGFKDSDDIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; SO4218; -.
GO; GO:005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0016874; F:ligase activity; IEA.
GO; GO:0008763; F:UPE-N-acetylmuramate-L-alamine ligase activity; IEA.
GO; GO:0009058; F:Dicsynthesis; IEA.
GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
                                                                                                                Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S., DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C., Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gabs
            MURC OR SO4218.
Shewanella oneidensis.
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.9%; Score 521.5; DB 16; Length
32.6%; Pred. No. 3e-28;
ive 87; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               488 AA; 53168 MW; DC45914D4869D353 CRC64;
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UDP-N-acetylmuramate--alanine ligase
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EMBL; AE015855; AAN57190.1; -.
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
                                                                                                 STRAIN=MR-1;
MEDLINE=22297686; PubMed=12368813;
                                                                                                                                                                                                                                                                                                                                                                                                   Pfam, PF01225; Mur_ligasë, I. -
Pfam, PF02875; Mur_ligase_C; 1.
TIGRFAMs; TIGR01082; murC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                     SEQUENCE FROM N.A.
                                                               NCBI_TaxID=70863;
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SEQUENCE FROM N.A.

STRAIN=RBSO / ATCC BAA-588;

CATAIN=RBSO / ATCC BAA-588;

MEDLINE=22827954; PubMed=12910271;

MEDLINE=22827954; PubMed=12910271;

A Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.,

A Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,

Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,

A Achtman M., Akin R., Baker S., Basham D., Bason N., Cherevach I.,

A Achtman M., Akin R., Toollins M., Cronin A., Davis P., Doggett J.,

Relingworth T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,

Betherl S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,

Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,

Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,

Mintehead S., Barrell B.G., Maskell D.J.;

"Comparative analysis of the genome sequences of Bordetella pertussis,

Rabinowits D. Carlesons and Bordetella bronchiseptica.";

BMEL, BR64449; CAR14511; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GAIVTSTAVAGDNPEVLAARAARIPVVPRAVMLAELMRLKRGIAVAGTHGKTTTTSLVAS 125
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                                                                                                                                                                                                                        Bordetella bronchiseptica (Alcaligenes bronchisepticus).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome. 468 AA; 49404 MW; 045E233D594FECFD CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate-allanine ligase (EC 6.3.2.8).
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31.7%; Pred. No. 3.2e-27;
PRT;
                                                                                                                                                                                                                                                                                                            Alcaligenaceae; Bordetella.
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Matches 145; Conservative
          PRELIMINARY;
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468 AA

PRT;

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Complete proteome.
PRELIMINARY;
                                                                                                                                                                                                                                                   Bordetella pertussis.
                                                                    01-0CT-2003
01-0CT-2003
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SEQUENCE
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Ameria D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.L.,
A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevan I.,
A Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevan I.,
A Chillingworth T., Collins M., Cromin A., Davis P., Doggett J.,
A Feltwell T., Goble A., Hamin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
Sharp S., Simmond M., Skelton J., Squares R., Squares S., Stevens K.,
Duwin L., Whitehead S., Barrell B.G., Maskell D.J.;
Comparative analysis of the genome sequences of Bordetella pertussis,
Bordetella paragerussis and Bordetella bronchiseptica.";
EMBL; BX640434; CAE39034.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186 MDTÝGHĎVARLKSAFIEFTQRLPFYGSAILCADDANVREIMPFVSRPITTÝGLSPDAQVC 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285 IKEALETFGGVKRRFNE----TTIANQ----VIVDDYAHHPREISATIETARKKYPHKE 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               304 İRBALAAFKGVGRRFTQWGDLPVPAAHGGGTFTLVDDYGHHPVEMAATLAAARGAWPQRR 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 VVAVFQPHTFSRTQAFLNEFABSLSKADRVFLCEIFGS------IRENTGALTIQDL 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 MVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYTSVAVTGAHGKTSTTGLLSH 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 AQDVQA--DGTRMRFTVQRRDRDVVLPALQVELNI.PGI.HNVRNALAAIAVATELGVDDAA 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 HYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALRNKGIKI-LPFDANNIKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 AQNIQITDKGTAFDVYVDGEFYDHFLSPQY-----GDHTVLNALAVIAISYLEKLDVTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43;
                                                                                                                                                                                                                                                                                                                                   Bordetella parapertussis.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.3%; Score 506.5; DB 16; Length 31.7%; Pred. No. 3.2e-27; Arive 75; Mismatches 195; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         468 AA; 49404 MW; 045E233D594FECFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            387 IDK -- IEGASLINEDSINVLEOFDNAVILFMGAGDIOK 422
                                                                            468 AA
                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=12822 / ATCC BAA-587;
MEDLINE=22827954; PubMed=12910271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 145; Conservative
                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                             MURC OR BPP3751
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
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DDT DDT DDT DDT DBT DBT SQ

RESULT 12

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SQUENCE FROM N.A.

STRAIN-Tohama I / ATCC BAA-589 / NCTC 13251;

KINDLINE=22827954; PubMed=12910271;

RADLINE=22827954; PubMed=12910271;

RADLINGWORTH T., Collins M., Churcher C.M., Bantley S.D., Mungall K.L., RADLINGWORTH T., Collins M., Cronin A., Davis P., Doggett J.,

RADLINGWORTH T., Collins M., Cronin A., Davis P., Doggett J.,

RADLINGWORTH T., Collins M., Cronin A., Davis P., Doggett J.,

RADLINGWORTH T., Collins M., Cronin A., Davis P., Doggett J.,

RADLINGWORTH T., Collins M., Cronin A., Davis P., Doggett J.,

RADLINGWORTH T., Whiter S., Sanders M., Saunders D., Seeger K.,

RADLINGWORTH S., Marrell B.G., Maskell D.J.,

Nomparative analysis of the gnome sequences of Bordetella pertussis,

REMEL; BX640420; CAE43293.1;

REMEL; BX640420; CAE43293.1;

REMEL; REMELS REMELS REMERS REMELS REMERS REMELS REMELS REMERS REMELS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS REMERS 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 IXEALETFGGVKRRFNE----TTIANO----VIVDDYAHHPREISATIETARKKYPHKE
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                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        468 AA; 49416 MW; 1E77233D4366E724 CRC64;
               01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
UDP-N-acetylmuramate-alanine ligase (EC 6.3.2.8).
MURC OR BP3022.
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(TrEMBLrel. 25, (TrEMBLrel. 25,
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Q87WY6;
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Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
Buell R., Uterback T., Van Aken S., Feldblyum T., Gwinn M.,
Berry K., Uterback T., Durkin A., Kolonay J., Madupu R., Daugherty S.,
A bodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
Mhite O., Fraser C., Collmer A.,
"Complete sequence of Pseudomonas syringae.";
"Complete sequence of Pseudomonas syringae.";
"Complete sequence of Pseudomonas syringae.";
"Complete sequence of Pseudomonas syringae.";
"Complete Sequence of Pseudomonas syringae.";
"Complete Sequence of Pseudomonas syringae.";
"Complete Sequence of Pseudomonas syringae.";
"Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

TIGR, PSPTO4407; -.
R GO, GO:000554; F:ATP binding; IEA.

GO, GO:000568; P:Bilgase activity; IEA.

R GO, GO:0009058; P:Diosynthesis; IEA.

InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR00410; Mur_ligase.

R InterPro; IPR06410; Mur_ligase.

R InterPro; IPR06410; Mur_ligase.

R InterPro; IPR06410; Mur_ligase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 HFVGIGGVGMCGIAEVLINLGYEVSGSDLKGSAVTE-RLESFGAQIFVGHRAENTVGADV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176 PDYFKDINDVFDAFQEMAHNVK-KGI-IAWGDDEHLRKIEADV--PIYYYGFKDSDDIYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIBGASLINEDSINVLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TFGGVKRRF---NETTI--ANQVIVDDYAHHPREISATIETARKKYPHKEVVAVFQPHTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                               Pseudomonas syringae (pv. tomato).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16; Length 486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----VILFMGAGDIQKLQNAYLDK---LGMKNA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          435 GVELAPLVKPLLRAGDILLCQGAGDIAGLAPRLLNSPLFVGAKVA 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 22.1%; Score 502; DB 16; Length 4 Best Local Similarity 33.1%; Pred. No. 7e-27; Matches 154; Conservative 80; Mismatches 193; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   486 AA; 52671 MW; 9020894E5F27C757 CRC64;
       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 25, Last annotation update)
UDP-N-acetylmuramate--alanine ligase.
MURC OR PSPTO4407.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01225; Mur_ligase; 1.
Pfam; PF02875; Mur_ligase_C; 1.
                                                                                                                                                                                                                                                                          Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ligase; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                   FROM N.A.
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                                                                                                                                                                                                                                                                                                           NCBI_TaxID=323;
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM 1
STRAIN=DC3000;
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Q83F17; 01-JUN-2003 (TrEMBLrel. 24,

PRELIMINARY;

Q83F17

RESULT 14 **Q83F17** 

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DH-PDYFKDINDVFDAF-QEMAHNVKKGIIAWG-DDEHLRKIEADVP--IYYYGFKDSDD 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 AQYRVVDYCQQG-----IQSLFQIH--SPQRKAPLTVKLSMPGQHNALNATAVTALADV 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHV-MNGDKKTSFLIG-----DGTGMGLPESDYFAFEACEYRRHFLSYKPDYAIMINIDF 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --GDHTVLNALAVIAISYL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  330 KYPHKEVVAVFOPHTFSRTOAFLNEFAESLSKADRVFLCEIF------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0016874; F:Iigase activity; IEA.
GO; GO:0009763; F:UP-N-acetylwiramate-L-alanine ligase activity; IEA.
GO; GO:00099058; P:biosynthesis; IEA.
GO; GO:0009273; P:cell wall biosynthesis (sensu Bacteria); IEA.
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MEDLINE=22606857; PubMed=12704232;

Seshadri R., Paulsen I.T., Eisen J.A., Read T.D., Nelson K.B.,

Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,

Nelson W.C., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,

Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,

Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;

"Complete genome sequence of the Q-fever pathogen, Coxiella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
Coxiellaceae; Coxiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 465;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) UDP-N-acetylmuramate--alanine ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
EMBL; AE016960; AAO89700.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000713; Mur ligase.
InterPro; IPR004101; Mur ligase_C.
Bem; PR01225; Mur ligase; 1.
Pfam; PP02875; Mur ligase; 2.
IGRPAMs; TIGR01082; murC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005758; MurC.
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SEQUENCE 465 AA; 50640
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                                                                                                                  Coxiella burnetii.
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                              NCBI_TaxID=777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 AIAVG--NELGVPDEAIVKALATFGGVDRRFQQYGEIPLPDQGGFALIDDYGHHPAEIAA 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               271 VIAISYLEKLDVTN--IKEALETFGGVKRRF---NETTIANQ---VIVDDYAHHPREISA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 TIETARKKYPHKEVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005737; C:cytoplasm; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0006874; F:ATP binding; IEA.
GO:0008763; F:UDP-N-acetylmurymate-L-alanine ligase activity; IEA.
GO:0009058; P:biosynthesis; IEA.
GO:0009058; P:biosynthesis; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 YAQNIQITDKGTAFDVYVDGEFYD----HFL-----SPQY-----GDHTVLNALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ol-oun-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MurC; UDP-N-acetylmuramate--alanine ligase protein (EC 6.3.2.8)
MURC OR NE0992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
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Pfam; PF01225; Mur_ligase.
Pfam; PF01225; Mur_ligase.
TREAMS; TIGR01082; murc;
Pfam; PF024975; Mur_ligase.
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   462 QTHG 465
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OM nucleic - nucleic search, using sw model

5, 2004, 22:02:04; Search time 5350 Seconds June Run on:

(without alignments)
10677.779 Million cell updates/sec

1 atgacacactatcattttgt.....gaaaaatgcgttttaagctt 1318 US-10-712-713-1 1318 Title: Perfect score: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6940544 Total number of hits satisfying chosen parameters: 3470272 seqs, 21671516995 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

GenEmbl:*

Database :

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is the number of results predicted by chance to have a Pred. No.

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ouery  1314 99.7 1335 6 AK742069 1214 99.7 1335 6 AK742069 1219 99.7 1335 6 AK742071 1314 99.7 1335 6 AK742071 1319 99.7 1335 6 AK742071 1319 99.7 1335 6 AK742071 1319 99.5 342600 1 AF003363 109.8 99.8 1332 6 AK671936 10.8 99.5 342600 1 AF003363 109.9 99.8 1314 6 AK671936 12.8 98.8 1314 6 AK191741 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6 B178031 1351 6	13 13 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	0 44		Length	82	1	escript
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5         1310.8         99.5 301550         1 AP0003134         AP0003134           6         1310.8         99.5 3022600         1 AP0003134         AP0003134           7         1309.2         99.5 372660         1 AP004828         AP004828           8         1314         1 AP034076         AP004828           8         1314         1 AP034076         AP004828           10         1293.2         98.1         1351         6 B35613         AP004828           11         1293.2         98.1         1351         6 B35614         AP0178030         AP004808           12         137.8         48.4         660         6 B35614         BD178031         BD178031         AP017033           14         48.4         660         6 B35614         AB017033         AB0170033         AB0170033 </td <td>1098765</td> <td>8</td> <td></td> <td>7</td> <td>φ,</td> <td>179</td> <td>7936</td>	1098765	8		7	φ,	179	7936
6         1310.2         99.5         342600         1 AP003363         AP003363         AP0043263           8         1314.0         1314.1         1 AP003363         AP004328         AP0043363           8         1312.1         1 AP004328         AP004328         AP004363           9         1302.8         98.8         1314.6         AP014014         AP014076           1         10.203.2         98.1         1351.6         BD178030         AP016448         AP016448           12         318.8         69.7         300029         1 AP017039         AP016444         BD178031           15         57.6         45.3         291804         1 AP017039         AP016474         BD178031           16         570.4         46.0         BD178031         AP016050         AP017039         AP0161674           17         570.4         42.0         30241         AP017039         AP016067         AP016067           20         553.4         42.0         30241         AP0460600         AP0160693         AP0160693           21         570.4         42.0         30241         AP0460600         AP041601         AP0160600           22         39.7         34980	100876	<u>.</u>		5	н,	131	03134
7         1309.2         99.3         272850         1 AP004828         AP004828         AP004828           7         1309.2         99.3         272850         1 AP004404         AP004828         AP004828           9         1302.8         98.8         1314         6 AX191741         AX191741         AX191741           10         1293.2         98.1         1351         6 BD178030         BD178031         BD178031         BD178031           13         637.8         48.4         660         BD178031         BD178031         BD178031           14         637.8         48.4         660         BD178031         BD178031         BD178031           15         637.6         45.2         300975         1 AB017033         AR017033         AR017033           16         597.6         45.2         300975         1 AR017033         AR017033         AR017043           17         570.4         43.3         610         AR134630         ARX13047         ARX13047           18         553.4         42.3         610         AR134630         ARX13047         ARX13047           20         553.4         43.3         610         ARX13047         ARX13047	110987	ė.		42	Н.	033	03363
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12         918.8         69.7         300229         1         AB016748         AB016748         AB016748           13         637.8         48.4         660         6         B35614         BD178031         AB017013         AB01600         AB01600         AB016000         A		÷.		n	9	33	3030 Mu
13         637.8         48.4         660         6         BB178031         BB5614         BB5614           14         637.8         48.4         660         6         BD178031         ABD178031           15         597.6         45.2         30075         1         AB017013         AB017013           16         45.2         30075         1         AB017013         AB017013         AB017013           17         570.4         43.3         619         6         AR194630         AB017013           18         553.4         41.4         29950         1         AB004600         AB016953         AB016953         AB016950           20         523         39.7         239980         AK413017         AB004600         AB169606           21         53.9         349980         AK413017         AK413017         AK413017           22         516.4         39.2         240050         AK413017         AK413017           24         39.2         349980         AK413017         AK413017           25         500.8         38.0         22060         AK413017           26         500.8         38.0         22060         AK41669	12	w.		000	ч	74	748 St
14         637.8         48.4         660         6         BD178031         BD178031           15         597.6         45.3         291804         1         AR017039         AR017039           16         596.         45.3         291804         1         AR017039         AR017039           17         570.4         43.3         619         6         AR194630         AR017045           18         553.4         41.0         302241         1         AR016953         AR016460           20         553.4         41.0         302241         1         AR016953         AR016460           20         553.4         41.0         202060         1         AL596169         AR016463           21         523         39.7         234980         6         AX413017         AX413017           22         516.4         39.2         246060         1         AL59109         AX413017           24         516.4         39.2         249080         6         AX4113017         AX413017           25         500.8         38.0         1092060         1         AL591099         AX413017           25         500.8         38.0         <	9	Υ.		099	9	E35614	5614 Murc
5   597.6   45.3   291804   1   AB017033   AB017033   AB017033   16   50.5   43.3   201975   1   AB017013   AB017013   AB017013   16   50.5   43.3   201975   1   AB016953   AB0194630   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953   AB016953	4	۲.		9	9	BD178031	3031
16   596   45.2   30075   1   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE017013   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702   AE01702	15	Υ.		918	ч	AE017039	7039 Bac
17         570.4         43.3         619         6         AR194630         AR194630           18         553.4         41.0         302241         1         AR016953         AR016953           19         553.4         41.0         302240         1         AL596169         AR016953           20         523         39.7         239950         1         AL596169         AR017045         AR017045         AR017045           21         523         39.7         349980         6         AX417045         AX413047           24         39.2         240050         1         AL591979         AX413047           25         500.8         38.0         220060         1         AL591979           26         500.8         38.0         220060         1         AR001518         AX413047           27         495.6         37.6         303250         1         AR001518         AX6011669           28         500.8         34.2         1         AX601265         AX601265           29         450.8         34.2         44.1         AX601265         AX601265           31         450.8         34.2         44.1         AX6012165	16	5		900		AE017013	701
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ALIGNMENTS

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Staphylococcus aureus Staphylococcus aureus Bacteria; Firmicutes; Bacillales; Staphylococcus.

Edwards,A., Dharamsi,A., Vedadi,M., Alam,M.Z., Awrey,D.,
Beattie,B., Domagala,M., Houston,S., Kanagarajah,D., Nethery,K.,
Bog.I., Mansoury,K., Mcdonald,M.L., Pinder,B., Viola,C. and
Wrezel,O.

REFERENCE AUTHORS

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                                                                                                                                       Length 1335;
                                                                                                                                    Query Match 99.7%; Score 1314; DB 6; Length 1:
Best Local Similarity 100.0%; Pred. No. 5.5e-190;
Matches 1314; Conservative 0; Mismatches 0; Indels
                                        Location/Qualifiers
1. 1335
Corganism="Staphylococcus aureus"
/mol type="genomic DNA"
/db_xref="taxon:1280"
Novel purified polypeptidés involved in
Patent: WO 03025007-A 27 27-MAR-2003;
Affinium Pharmaceuticals Inc. (CA)
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Kunsch, C.A., Choi, G.H., Barash, S., Dillon, P.J., Fannon, M.R. and Rosen, C.A.
                                                                                                                                                                                                                                             1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
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Novel purified polypeptides involved in membrane biosynthesis Patent: Wo 03025007—A 29 27-WAR-2003
Patent: Wo 03025007—A 29 27-WAR-2003
Affinium Pharmaceuticall, Inc. (CA) CATCAATTGAAATTAGAAGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA CATGTTATGAATGGTGATAAAAAGGCTTCATTTTTAATTGGTGATGGCACAGGTATGGG TATAAACCTGATTACGCAATTATGACAAATATTGATTTGGATCATCCTGATTATTTAAA TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA GITGCICITAGAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAGAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATGATCAA TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACIICIACAACAGGIITAITAICA TIGCCTGAAAGTGATTATTCGCTTTTGAGGCATGTAATATAGACGTCACTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAAATC 22 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT 6; Length 1335; 0; linear Indels Staphylococcus aureus Bacteria; Firmicutes; Bacillales; Staphylococcus. aureus" Query Match 99.6%; Score 1312.4; DB 6
Best Local Similarity 99.9%; Pred. No. 9.6e-190;
Matches 1313; Conservative 0; Mismatches 1; DNA 1335 bp WO03025007. /organism="Staphylococods /mol_type="genomic_bnA" /db_xref="taxon:1280" 29 from Patent AX742071.1 GI:30524567 Staphylococcus aureus Staphylococcus aureus 661

1161 1020 1101 1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 1140 1021 CAACCACACATTCTCTAGAACACAGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1080 960 900 540 600 999 681 720 741 780 801 840 861 420 480 561 621 501 180 240 300 360 381 441 120 141 201 261 321 GAAACTACAATIGCAAATCAAGTIATIGTAGATGATTATGCACACCATCCAAGAGAAATT 961 AGTGCTACAATTGAAACAGCACGAAAGAATATCCACATAAAGAAGTTGTTGCAGTATTT ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATCAAATTACGGATAAAGGT ACIGCITITICATICICIATICICATICICACATITIATICATCACTICCICICICCICACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAAACGTCGTTTCAAT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT GATATTAATGATGTTTTTTGGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAAGGTATT TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTAAGT ATGCATGATTTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTAGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACITCAGTAGCIGTAACTGGTGCACATGGTAAAACTICTACAACAGGTTTATTATCA CATGITATGAATGGTGATAAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA CATGTTATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-JAN-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; Zfonee 49-10 Nighihara, Shibuya-ku, Tokyo 151-0066, Japan Center; Zfonee 49-10 Nighihara, Shibuya-ku, Tokyo 151-0066, Japan Tel:mail:biosaite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1593, Pass:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701258.
                                                                                                                                                                                                                                                                                                                   AP003134 301550 bp DNA linear BCT 24-APR-Staphylococcus aureus subsp. aureus N315 genomic DNA, complete
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Submitted (30-JAN-2001) Director-General, Biotechnology Cente

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                                                                                                                                                                      1282 CAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTT
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AP003134 BA000018
AP003134.2 GI:14349226
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SNHDI QHYINYLIKLGYPLETITDI DFBTI XQYMLSDKRNDKQGVQMVLI KHFGDI VV
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291118 AIGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 291059
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                                                                                                                                                     CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA
                                                                                                                                                                                                                                                                                           290878 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA
                                                                                                                                                                                                                                                                                                                                                            290818 TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA
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Gaps

Query Match
99.5%; Score 1310.8; DB 1; Length 301550;
Best Local Similarity 99.8%; Pred. No. 3.5e-190;
Matches 1312; Conservative 0; Mismatches 2; Indels 0; G;

us-10-712-713-1.rge

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (4782. .5657)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (4782. .5657)
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                                                                                                                                                                                                                                                                                                                       note="SAV1630"
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                          290038 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 289979
                                                                                                                                              289919
                                                                                                                                                                                                                                                           Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College Submitted (28-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology 1-1-1 Ten-nopdai, Tsukuba, Ibaraki 305-8577, Japan Temail:tohta@sakura.cc,fsukuba.ac.jp, Tel:81-298-53-3454, Fax:81-298-54-3454)
On May 29, 2004 this sequence version replaced gi:13875943.
                                                                                     1201 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTATGGGTGCAGGTGATATT 1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuroda, M., Ohta, T., Uchiyama, I., Baba, T., Yuzawa, H., Kobayashi, I.,
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Shiba, T., Hattori, M., Ogasawa, Hayashi, H. and Hiramatsu, K.
Whole genome sequencing of meticilla resistant Staphylococcus
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complement (1029. .1130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BCT 24-APR-2003
                                                                                                                                                                                                                                                                                                                                                 289858 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 289805
                                                                                                                                              AP003363 342600 bp DNA linear BCT 24-APR.
Staphylococcus aureus subsp. aureus Mu50 genomic DNA, complete
1261 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTAA 1314
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Bacteria, Firmicutes, Bacillales, Staphylococcus.
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Staphylococcus aureus subsp. aureus Mu50
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AP003363 BA000017
AP003363.2 GI:14247399
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TITLE

SOURCE

FEATURES COMMENT

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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DCYALLGLVHTLAKEMPGRFKDYIAMPKQNLYQSLHTTVVGPNGDPLEIQIRTFDMHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                          KNGLPYIMHPIQVAGILTEMRLDGPTIVAGFLHDVIEDTPYTFEDVKEMFNEBVARIV
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complement (6118. .8307)
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                                                                         /gene="relA"
complement(6118.
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                                                                                                                                                              132739 Aridcardarinagaacardaagricaagarcgararrgagaacracgrarrracagaa
                                                                                                                                                                                                                   GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA
                                                                                                                                                                                                                                                                                   GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
                                                                                                                                                                                                                                                                                                                                                 TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA
                                                                                                                                                                                                                                                                                                                                                                                                                   132499 TATACTICAGTAGCIGTAACIGGTGCACAIGGTAAAACTICTACAACAGGITTAITATCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132259 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132139 TATGGATTTPAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
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                                                                                                                                  ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA
                                                                                                                                                                                              GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA
                                                                                                                                                                                                                                                                                                                               CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132199 ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGCTCCAATTTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132019 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
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                                                                   IGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
                                                                                                                                                                                                                                                                GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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                                     Gaps
      Length 342600;
                                     0;
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      1;
 Score 1310.8; DB 1
Pred. No. 3.3e-190;
0; Mismatches 2;
99.5%;
                Similarity 99.8
12; Conservative
Query Match
Best Local Simi:
Matches 1312; (
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1021 CAACCACACATTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1080

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NAGTKILPPDANNIKEDWVVIQGNEASSHERIVRAHQLKLDVVSYNDFLGQIIDQYT
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BEDGATNKESEYSGGOLDDEBPYSLINTEABENTYSNIEDNITRNASSERTUDAPKTÜGH
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VYTGPSVTRFELSVEKGYVCKSRIPLADDINFALAAKUIRTBAPIPSTSVGETSVN
QUPTTVNLBSIIESPFKNAESKLTVAMGYRINNEPLLADIAKTPHALIAGTGSGKS
VCINSILMSLLYKNHPBELRILLIDPKMVELAPYNGLPHLVAPVITDVKAATQSLKWA
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KAQKARGGIHMIVATQRESVNVITELIKANIPRILAFRAFAPTESSUDSKTILDSGABER
LLGYGDMLYLGSGMWFFIRVGTFVSDDEIDDVVDFIKQQRREPYLFERKELLEKKTQT
QSQDELPDDVCAFMVNEGHISTSLIQRHPQIGYNRAARIIDQLEQLGYVSSANGSKPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="DNA translocase stage III sporulation prot homolog ORFID:MW1684"
                                                                                                                                                                                                         lypothetical protein, similar to general stress protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_gtart=1
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                                                               complement (1907. .2398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="murc"
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                                                                                                                                                gene="MW1682"
'note="ORFID:MW1682
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QKQAKLTPGSKESQLTEALFAEKPVAKNDLKEIPQLVTKKNDVSESETVNIDNKDTVK
QKEAKFENGVITRKADEKTTNNTAVDKKSGKQSKKTTPSNKRNASKASTNKTSGQKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jy Center, Aoki, K., Oguchi, A.,
Baba, T., Kuroda, M., Hiramatsu, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center; 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131539 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 131486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Baba,T., Takeuchi,F., Kuroda,M., Yuzawa,H., Aoki,K., Oguchi,A., Nagai,Y., Iwama,N., Asano,K., Naimi,T., Kuroda,H., Cui,L., Yamamoto,K. and Hiramatsu,K.
Genome and virulence determinants of high virulence
                                                                                          AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                                                                                                                                                                                            1261 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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Nagai,Y., Agano,K., Iwama,N., Ba
Kikuchi,H.
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961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1020
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                                                                                                                                                                                                                                          3785 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3605 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3245 GAIATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT
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                                                                                           1; Length
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/product="conserved hypothetical protein"
                                                                                                                                            Indels
                                                                                           Score 1309.2; DB 1
Pred. No. 6.2e-190;
0; Mismatches 3;
                                                                                                                                                                                          ATGACACACTATCATTTTGTCGGAATTAAAGGTT
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ilarity 99.8%;
Conservative
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Best Local Simil
Matches 1311; C
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                      /codon gtatt=1
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ASSGMICSMKELNLPNAPEEKGINVLNDSYEIGQAFPE"
complement (8279. 9136)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MATFQMRDKLKERLSHLDVDFKFNREBETLRIYRTDNNKGITIK
INAIVAKYEDKKEKIVDEIVYYUDALAQMADKTLESISSOLMPVIRATSFDKKTKÖ
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TYDEVKGNTFYFINSNGYYDASRILMTAFLABIEAQCQEMUNAVPHQDVLITADIRN
KTGYDVMAHLTMEFFTKGLVPITSLSFGYKQGHLEPIFILGKNNKQKRDPNVIQRLEA
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QRLVIKNRNGDKIIGVVSNIPKHFRTGSBGAPEIKDLFLIGAQNBDBSVRERGIDIGD
TIV PHTPFFIQLSEHRYSAKMDNRYGCVLAIELLELLKDIELDVDLYVGANVQBEVGL
RGAKASAEMIDPDVAFVVDCSPANDVKGSQPLSGELGKGTLIRIKOTMILKPYFRDY
LLKLVEAHDIEHQYYMSPGGTDGGEIHKANIGIPTAVIGVCARYIHSTDSVFDIRPY
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PMFDFVSVDRDKFWDICIENGIMGIPSFLVYKNGELLGSYIGKERKSIEQIDAFLAQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ORFID:MM1688
dod-1,4-beta-glucanase homolog"
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                                                                                                                                                                                                                                                                                                                                                                                         product="conserved hypothetical protein"
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/db_xref="G1:21204856"
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/codon_start=1
/transl_table=11
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'note="ORFID:MW1686"
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SVAYTGAHGKTSTTGLLSHVMGDKKTSFLIGDGTGMGLPESDYFAFEACSTRAFLS
YKEDYALMYNIDPEDPPYFKDINDVFDAFQENAHNVXKGIIMMGDDEHLRKIEADVPT
YYYGFKOSDDIYAMYNIOTDTMGTAFDYVVDGEFYDHFLSPQYGDHTVLNALAVIAISY
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                                                                              AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                           AAAGCAGATCGTGTATTCTTATGTGAAATTTTTTGGATCAATTAGAAAAAATACTGGCGCA
                                                                                                                               AGTGCTACAATTGAAACAGCACGAAAGAATATCCACATAAAGAAGTTGTTGCAGTATTT
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/organism="Staphylococcus
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Antisense antibacterial/cell division composition and method Patent: WO 0149775-A 23 12-JUL-2001;
Avi Biopharma, Inc. (U$)
Location/Qualifiers
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15-OCT-2002
25-DEC-2001 JP 2001391079
03-JUL-1997 US 60/052720
NICOLA G WALLIS,MARTIN K R BURNHAM
C12N1S/09,AGIK31/7088,AGIK38/43,AGIK38/55,AGIK45/00,AGIK48/00,
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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM PLC
OS Unidentified
PN JP 2002300888-A/1
PD 15-OCT-2002
PP 25-DEC-2001 JP 2001391079
PR 03-JUL-1997 US 60/052720
PI NICCLA G WALLIS, MARTIN K R BURNHAM
PC C12N15/09, A61K31/7088, A61K38/43, A61K38/55, A6
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                                                                                       Extent: JP 1999225773-A 1 24-AUG-1999;
SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
OS Unidentified
PN 1999225773-A/1
PD 24-AUG-1999
PF 03-JUL-1998 UP 1998225115
PR 03-JUL-1997 US 66/052720
PR NICOLA G WALLIS, MARTIN K R BURNHAM
PC CIZNIS/09, A6IK31/70, A6IK38/53, A6IK39/55, A6IK39/395, PC
A6IK39/395,
PC A6IK39/395,
PC A6IK39/395,
PC G12NIS/09, A6IK48/00, C07K16/40, C12NI/21, C12P21/02, C12P21/08, PC
C12Q1/68,
PC G01N33/566//(C12NI5/09, C12R1:445), (C12NI/21, C12R1:445), PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98.1%; Score 1293.2; DB 6; Length 1351; llarity 99.0%; Pred. No. 7.8e-187; Conservative 0; Mismatches 13; Indels 0;

    1. 1351
    /organism='Unidentified'

                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                          PC G01N33/566//(C12N15/09,C12R1:445)
C12N15/00,A61K37/60,
PC A61K37/64,(C12N15/00,C12R1:445)
CC Strandedness: Double;
CC Topology: Linear;
FH Key
FT Source Lossinn Coalifie:
FT FOURCE COARDONES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:32644"
                                                          Nicola, G.W. and Martin, K.R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                          (bases 1 to 1351)
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35613
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Best Local Simil
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Staphylococcus epidermidis ATCC 12228, section 5 of 9 of the ADOI6748 ASOI67929
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Staphylococcus epidermidis ATCC 12228

Staphylococcus epidermidis ATCC 12228

Bacteria; Firmicutes; Bacillales; Staphylococcus.

E 1 (bases 1 to 300029)

S Zhang, Y., Ren, S., Li, H., Fu, G., Lu, L., Lu, G., Jia, J., Tu, Y., Qin, Z., Chen, Z. and Wen, Y.

Direct Submission

L Submitted (05-NOV-2002) Chinese National Human Genome Center at Shanghai, 250 Bi Bo Road, Shanghai 201203, China

Location/Qualifiers

1. 300029

I. 300029 als Bo Road, Shanghai 201203, China

Location/Qualifiers

// Organism="Staphylococcus epidermidis ATCC 12228"

// Organism="Staphylococcus epidermidis ATCC 12228"

// Ab_xref="ATCC:12228"

// Ab_xref
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                                                                                                                   GGTGACCATACAGTTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
                                                                                                                                                                                                   GATGTTACAAATATTAAAAGCATTAGAAACGTTTGGGGGTGTTAAAACGTTCAAT
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                          ACTGCTTTTGATGTGTATGTGGATGTTTTTTATGATCACTTCCTGTCTCCACAATAT
                                                                                  GGTGACCATACAGTTTTAAATGCATTAGCTGAATTGCGATTAGTTATTTAGAGAAGCTA
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/protein id="AA004767.1"
/db_xref="GI:27315632"
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/locus tag="SE1168"
/codon_start=1
/transT_table=11
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                                                                                                                                    Cl2N5/10,
PC C12P21/02,C12Q1/02,C12Q1/68,G01N33/15,G01N33/50,C12N15/00, PC C12N5/00,
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A61P39/02,A61P43/00,C07K14/195,C12N1/15,C12N1/19,C12N1/21, PC
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AGIP7/02, AG1P9/00, AG1P11/00, AG1P13/02, AG1P13/12, AG1P17/00, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTTATGATCACTTCCTGTCTCCACAATAT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                        A61P19/02, A61P19/08, A61P21/00, A61P25/00, A61P27/00, A61P29/00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       442 TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT
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                                                                                                                                                                                                                                                                                                             ce 1. 1351
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1293.2; DB 6
Pred. No. 7.8e-187;
                                                                                                                                                                                                                                                                                     Location/Qualifiers
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MurC
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99.0%;
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Best Local Similarity 99.0
Matches 1301; Conservative
                                                                                                                                                                                                                                                                                                                      source
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/ETABLALIAN PARKINSVVIKLMLTILLIVATVLILLSVSLITFLQYYFTQETEN
AIKEDARKILSSUVERKHWKTLALONSQTLLIGYPOMSEKEDSSYKOTKKQ
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VBSELGKGTSFIIRLPKSQYGIS"

COMDIEMENT (8766. .9491)

// LOCUE LAGE LAGE 1821176"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="ribosomal large subunit pseudouridine synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'transI_table=11
'product="staphylococcal respiratory response protein
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complement (7016. .8782)
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transl table=11
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Complement (2795. . 4174)
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RETPETNVENCYIAGVIAAGNDANTIFIENGKYHGGVITQSILTKKQTPLET"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / LTAIN BLAID TO MANAGONIA KRWPGPDEFKEGGEIIDSVIHGRHTLGILPTGSGKSI.
CYQLPTVILEKPTLISPLISLANDOWGTKAKGETHVACVISGMDEVERDNIKRLS
KSRFIYLSPEYILGPRYALISPLISLANDOWGTKAKGETHVACVISGMDEVERDNIKRLS
KSRFIYLSPEYILGPRYALISPLIANIA MANAGORINEN SEMGYDPRPHYALVGKIIHHF
NSATVLATARARSPORNEN TAININGELSVINGEN SEMGYDPROBGSKIEWIL
PPLSNSGPTIIVSSKKRCLELAQMIYDSSYLLOGIGRAGORINGSSIRGENDIP
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ILETLIATU ITVDDITTWEFTGNHLPDEKEKILSTAN GOFTSGLADI THQSYGRKAL
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FINYYQKHRGFRLKFYKEHFTDWTYFQIKLVIVGIERGDLIABR"
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translation="MOTIESIIIGGGPCGLSAAIEQKKKGIETLVIEKGNVVESIYNY
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AEVPEELYEDMEDALEGCPTDSIKIEDEPFDGDALKFE"
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complement (4161, .5123)
/locus tag="SE1171"
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complement (1256. 2674)
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complement (5572. .5676)
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'transl_table=11
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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP PUBLIC LTD CO
S Unidentified
PN 1999225773-A/2
PD 24-AUG-1999
PF 03-JUL-1998 JP 1998225115
PR 03-JUL-1997 US 60/052720
PI NICOLAG WALLIS, MARTIN K R BURNHAM
PC C12N15/09, AGLK31/70, AGLK38/53, AGLK39/085, AGLK39/395,
PC AGLK39/395,
PC AGLK39/395,
PC AGLK48/00, AGLK48/00, C07K16/40, C12N1/21, C12P21/02, C12P21/08, PC
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247865 TATGGCTTTAAAGAAACAGATGACATCTATGCTAAAAAATATTCAAATTACTGAAAAGGGT
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                                                                                                                    ACTGCTTTTGATGTGTATGTGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT
                                                                                                                                                                                                                                                                              781 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTTAGAGAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                   841 GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247685 AATGTAGAAAATATTAAAGAAGCACTGATAACATTTGGTGGTGTAAAACGTCGTTTTAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247505 CAACCACATACGTTCTCAAGAACTCAAGCATTTTTAAACGAATTTGCTGAGGTTTAAGT
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C12N15/00,A61K37/60,
PC A61K37/64,(C12N15/00,C12R1:445)
CC Strandedness: Double;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                               /organism="unidentified"
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    .660
    /organism='Unidentified'.

                    Location/Qualiflers
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                                                                         1. .660
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/mol_type="genomic DNA"
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Wallis, N.G. and Burnham, M.K.R.
Murc
                                                             Location/Qualifiers
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BD178031.1 GI:30015295
JP 200230088-A/2.
unidentified
     Topology: Linear,
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Best Local Similarity 98.9°
Matches 642; Conservative
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TITLE
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ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS JOURNAL

TITLE

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| Da xref="G1:30253119"
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VRLSPTIDEHDFNTKLRNAIKFLEKGDKVKASIRFKGRAITHKEIGQRVLDRFSEACA
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complement(3876. 4757)
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PID:1805280, PID:537331, PID:829111, and PID:836669;
identified by sequence similarity; putative"
                                                                             /note="similar to SP:P55874; identified by sequence similarity; putative"
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/note="similar to SP:P55872; identified by sequence similarity; putative"
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/transT_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="similar to SP:P18255; identified by sequence similarity; putative" codon start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="conserved hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthetase"
                                                                                                                                    /codon_start=1
/transl_table=11
product="ribosomal_protein_L35"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="threonyl-tRNA s
/protein_id="AAP28509.1"
/db_xref="GI:30259321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="thrs-2"
/locus_tag="BA4820"
complement(1632, .3569)
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                                                                                                                                                                                                                                                                                                                                                          /gene="infC"
/locus_tag="BA4819"
complement(735. .1295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1632. .3569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKSETIALDAFVDMIKVEGKR"
                                                                                                                                                                                                                                                                                                                                      complement (735. .1295)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /locus tag="BA4820"
                                                      locus tag="BA4818"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (3876.
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/trans1_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="thrs-2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="infC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I.,
Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E.,
Okstad, O., Helgason, E., Rilsfone, J., Wu, M., Kolonay, J., Beanan, M.,
Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madup, R., Daugherty, S.,
Burkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H.,
Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J.,
Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A.,
Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapple, E., Okstad, O., Helgason, E., Rilerone, J., Wu, M., Kolonay, J., Beanan, M., Dodson, R., Brinka, L., Gwinn, M., DeBoy, R., Madupu, R., Daugherty, S., Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H., Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J., Cline, R., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and
                                                                                                                                                                                                                        BCT 30-APR-2003
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YAFRDRRQKKRDFRKLWITRINAAARMNGLSYSRLMHGLKNAGIEVNRKMLADLAVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The genome sequence of Bacillus anthracis Ames and comparison to closely related bacteria
Nature 423 (6935), 81-86 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission Submitted (26-MAR-2003) The Institute for Genomic Research, 9712
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'note="identified by match to PFAM protein family HMM
                                                                                                                                                                                                                  AE017039 291804 bp DNA linear BCT 30-AFF
Bacillus anthracis str. Ames section 16 of 18 of the complete
                    ATTACAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTTTAA 1314
                                                 601 ATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA

    .291804
    /organism="Bacillus anthracis str. Ames"

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'db_xref="GI:30259318"
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/strain="Ames"
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complement(119. .475)
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complement(119..475)
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/locus_tag="BA4818"
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AE017039 AE016879
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YKLEQEYQMFIETLRQQVRSRKSRLSCVHLIFDESFIFYDDKGRRLKQEKLVRYMDED
LLKQKDVYIDTKVIAPLLSISPKKIYLYTKEQDHNMIITLRNVPQERVQLHGLHEFER
                                                                                                                                                                                                                                                                        translation="MEHIQNSFAKLMENENFKNRYEVLKAEVMAHPRVKEFIDEHRGE"
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RKVAYDERKKYEKLVQSVYMPTDILQATMENIDPSDLDARIDAIGAANEFISAYEPGK
KVQGLYLYGKRGVGKTYLLGAIANELARKKISSMLVYFPBFLREIKSSIQDNSIGEKI
DAVKRVQVLMLDDIGARAMSSFVRDDVLGAILQFRMLENLPTFFTSNFDFKQLEHHLT
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SFNDVFGSFNPGQLEHAQEDLRIPKTTAMPSNEKGDAPKVWNDFFDFSLFVDGLSALV
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AKEENROY QEWAETKKKGRI SKKTVRKEMV PDMLKEEPKEQEKETVKKDASAEKGAST
LEDERKRLEEVLKKYKRD."
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GQALPVLSERVQPHAARWMKEKEPSTQEEMLIKQLEEISPKQLLKEISGGAEATKADL
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ELRDIDDVAYVRFASVYRQFKDLNVFIEELKDILQKERE"
                                                                                                                           /iocus tag="BA4822"
/noce="almilar to GB:X57110, GB:X69207, SP:P22681,
PID:29731, GB:X57110, GB:X69207, SP:P22681, and
PID:29731, identified by sequence similarity; putative"
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/transl_table=11
/product="DNA replication protein DnaB"
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                                                                                                                                                                                                                         'product="primosomal protein Dnal"
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Pred. No. 4.8e-
0; Mismatches
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/locus tag="BA4824"
/note="identified by match
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/gene="dnaB"
                                                complement (5038. .5976)
                                                                                                                                                                                                                                          /protein_id="AAP28511.1
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complement(8291. .8683)
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                               NVKNLKNKGNALDFLSF"
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/transT_table=
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                                                                gene="dnaI"
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larity 66.4%;
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Best Local S:
Matches 858
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ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC

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                                                                                                                                                                                                                                                      102931 GGACAAGTGATTGCAGGAATGCATTTCCTGATACGCATGAAGAAATCGTAGCAGCA
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                                                              GTTGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAGAA
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                                                                                                                                                                                           GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
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Search completed: June 6, 2004, 01:40:50 Job time : 5358 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June Run on:

6, 2004, 02:44:45; Search time 635 Seconds (without alignments) 8817.520 Million cell updates/sec

US-10-712-713-1 Perfect score: Title:

1 atgacacactatcattttgt......gaaaaatgcgttttaagctt 1318 Sequence:

Gapop_60.0 , Gapext 60.0 OLIGO NUC Scoring table:

3373863 seqs, 2124099041 residues Searched:

50 Word size :

35 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

N_Geneseq_29Jan04:* 1: geneseqn1980s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2003as:* geneseqn2003bs:* 9епевефп2003св:∗ geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2002s:* Database:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn20048:*

SUMMARIES

Result		Query				
No.	Score	Match	Length	DB	A	G
ļ	1318	100.0	1318	4	AAS00189	Aas0018
7	1314	99.7	1335	σ	ADD15462	Add1546
m	1311	99.5	1332	7	ACF72770	Acf7277
4	1263	95.8	1335	σ	ADD15464	Add1546
2	1212	92.0	1314	_	ACA19726	Aca1972
9	957	72.6	1335	4	AAS54558	Aa85455
7	954	72.4	1311	4	AAS51660	Aa85166

SG	Score	Match	Match Length DB	8	ID	Description	
	1210	1 0		# 0	AASUULBS		aureus
	# 1		_	ע	AUU15462		Stapnyloc
	1311	99.5	1332	7	ACF72770	Acf72770 St	Staphyloc
	1263	95.8	1335	σ	ADD15464	Add15464 St	Staphyloc
	1212	92.0	1314	7	ACA19726	Aca19726 Pr	Prokaryot
	957	72.6	1335	4	AAS54558		Staphyloc
	954	72.4		₹	AAS51660	Aas51660 St	Staphyloc
	842	63.9	1351	7	AAV99650	Aav99650 UD	UDP-N-ace
	740	56.1	2424	N	AAV74703	Aav74703 St	Staphyloc
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	275	20.9	613	~	AAV53479	Aav53479 DN	DNA encod
	257	19.5	5 257	4	AAS50351	Aas50351 St	Staphyloc
	257	19.5	5 257	7	ACA17633	Aca17633 Pr	Prokaryot
	225	17.1	225	4	AAS49022	Aa849022 St	Staphyloc
	225	17.1	225	4	AAS49054	Aa849054 St	Staphyloc
	225	17.1	225	4	AAS49060	Aa849060 St	Staphyloc
	225	17.1	225	4	AAS48994	AaB48994 St	Staphyloc
	225	17.1	225	7	ACA16308	Aca16308 Pr	Prokaryot
	225	17.1	225	_	ACA16221	Aca16221 Pr	Prokaryot
	225	17.1	. 225	7	ACA16304	Aca16304 Pr	Prokaryot
	225	17.1	225	7	ACA16261	Aca16261 Pr	Prokaryot
	206	15.6	206	4	AAS48839	Aas48839 St	Staphyloc
	206	15.6	206	7	ACA16071	Aca16071 Pr	Prokaryot

Aca16230 Prokaryot Aa851038 Staphyloc	Aas50998 Staphyloc Aca18282 Prokaryot	Aca18280 Prokaryot Aas50478 Staphyloc	Acal 7740 Prokaryot	Aaa26910 Essential Aaf91592 Staphyloc	Aas08061 Staphyloc	Add67439 Antibacte	Ade73663 Mutant ba
ACA16230 AAS51038	AAS50998 ACA18282	ACA18280 AAS50478	ACA17740	AAA26910 AAF91592	AAS08061	ADD67439	ADE73663
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227 158	158 158	158	143	888	888	888	888
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## ALIGNMENTS

RESULT 1 AAS00189

AAS00189 standard; DNA; 1318 BP.

AAS00189;

(first entry) 04-JUL-2001

S. aureus DNA encoding UDP-N-acetylmuramate:L-alanine ligase, MurC.

UDP-N-acetylmuramate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyelitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis; 

Staphylococcus aureus.

Location/Qualifiers "Murc" 'product= 1. .1314 /*tag= a

WO200116292-A2

08-MAR-2001.

31-AUG-2000; 2000WO-US023773.

(HUMA-) HUMAN GENOME SCI INC.

99US-0151933P.

01-SEP-1999;

Choi GH;

WPI; 2001-183259/18. P-PSDB; AAU00828 New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.

Claim 1; Page 14; 225pp; English.

an ligase). The polymucleotides of the invention are used to detect
ligase). The polymucleotides of the invention are used to detect
Staphylococcus nucleic acids in a biological sample from an animal for
diagnosing Staphylococcus infections. The polypeptides of the invention
are used to detect anti-Staphylococcus antibodies in a biological sample
from an animal to diagnose Staphylococcus infections. The polypeptides
are also used in vaccines to elicit protective antibodies in an animal to
a member of the Staphylococcus genus and for preventing or attenuating an
infection caused by a member of the Staphylococcus genus e.g wound
infection, cellulitis, burn infection, eyelid infection, food possoning,
joint infection, neonatal conjunctivitis, osteomyelitis, skin infection,
scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's The sequence encodes S. aureus MurC (UDP-N-acetylmuramate:L-alanine

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disease and Lyell's disease), toxic shock syndrome and endocarditis. The polynucleotides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in vivo diagnostic and therapeutic methods
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8 %	1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 114
& A	1141 TTAACGATACAATTTAATTGATAAAATTGAAGGTGCATCGTTAATTAA
ර් සි	1201 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTTA
දි දි	1261 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAAGCTT 1318 
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XS	obeln accolumnamace aramine ilyane. Staphylococcus aureus.
XEEEE	Key Location/Qualifiers CDS 1. 1335 Atag= a /product= "MurC protein"
XEX	WO2003025007-A2.
EXE	27-MAR-2003. 20-SEP-2002; 2002WO-CA001428
X X X X X X X X X X X X X X X X X X X	21-SEP-2001; 2001US-0323992P. 21-SEP-2001; 2001US-0324152P. 25-SEP-2001; 2001US-0324692P. 26-OCT-2001; 2001US-0339924P. 29-OCT-2001; 2001US-0339924P. 30-OCT-2001; 2001US-033966F. 18-DEC-2001; 2001US-033966F. 18-DEC-2001; 2001US-0341776P. 18-DEC-2001; 2001US-0341776P. 18-DEC-2001; 2001US-0341776P.
XX PI PI	Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B; Domagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansoury K; Mcdonald M, Pinder B, Viola C, Wrezel O;

us-10-712-713-1.oligo.rng

Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria. WPI; 2003-468119/44. P-PSDB; ADD15463

Claim 20; SEQ ID NO 27; 325pp; English

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), CS Exreptococcus pneumoniae (S. pneumoniae) and Escherichia coli (B. coli) that provide novel antimicrobial targets. Specifically, it refers to colypeptides that are involved in membrane biosyntheeis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also characterisation by labelling with isotopic or heavy atoms, and also information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectants, food products to eliminate potential pathogens. This polynucleotide sequence is DNA predicted from the genomic sequence of S. aureus UDP-N-acetylmuramate-alanine ligase (murc) of the invention. 

Sequence 1335 BP; 472 A; 161 C; 255 G; 447 T; 0 U; 0 Other;

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480 240 360 420 541 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT 600 201 261 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 300 321 381 441 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 540 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 141 501 502 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 561 81 TATACTICAGIAGCIGIAAACIGGIGCACAIGGIAAAACTICIACAACAGGIITAATIAICA CATGTTATGAATGGTGATAAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA ATGACACACATTTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA GTTGCTCTTAGAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAATGTTAATGATTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TIGCCTGAAAGTGATTATTTCGCTTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA Gaps . 0 DB 9; Length 1335; Indels ·, 99.7%; Scor. 100.0%; Pred. No. v, ... 0; Mismatches Query Match
Best Local Similarity 100.
Matches 1314; Conservative 481 121 142 241 301 22 61 82 181 202 361 382 421 442 262 322

1020 1200 1260 1080 1221 1281 1101 1161 1041 960 720 741 780 801 861 900 921 981 562 GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT icidilitidilitidilitidilitidilitidilitidilitidilitidicatecengiceceaaatat GABACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT **TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTTCAAATTACGGATAAAGGT** ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTTATGATCACTTCCTGTCTCCACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT 961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 1021 CAACCACACATTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1042 CAACCACACACTTTCTCTAGAACACAGGCATTTTTTAAATGAATTTGCAGAAAGTTTAAAGT 1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATTACTGGCGCA 1222 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTATTATGGGTGCAGGTGATATT CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1335 Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis; enzymatic assay; antibiotic target gene; ds. BP Staphylococcus aureus DNA #450. ACF72770 standard; DNA; 1332 27-MAR-2002; 2002WO-IB002637. 27-MAR-2001; 2001GB-00007664 (first entry) Staphylococcus aureus WO200294868-A2 20-NOV-2003 28-NOV-2002 682 601 1141 721 781 802 841 901 922 1102 1201 1261 1282 661 ACF72770 ACF72770 ID ACF7 XX RESULT 3 심 ద 셤 qq 셤 셤 à ਨੇ ð ð 셤 ò 8 엄 ò 8 셤 ò 셤 셤 ð à ò

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                                                                                                                                                            The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an autibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of
                                                                                                                                                                                                                                                                                                                                                                                                                ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120
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                                                                                           protein, useful as a vaccine for treating or infection, specifically an infection caused by
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                                                                                                                                                                                                                                                                                                                     Score 1311; DB 7; Length 1332;
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                                                                                                                                                                                                                                                                       novel S. aureus genes of the invention
                                                                                                                                        Claim 6; SEQ ID NO 899; 49pp; English
                                   Σ
                                  Scarselli
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                                                                                           New Staphylococcus aureus
preventing Staphylococcal
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Matches 1311; Conservative
                                                                                                                 S. aureus, e.g. sepsis.
                                   Mora M,
                                                         WPI; 2003-120786/11.
            CHIRON SPA
                                                                    P-PSDB; ABM71210
                                  Masignani V,
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622 ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 681
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                                                                                                   TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT
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/product= "MurC protein"
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20-SEP-2002; 2002WO-CAUTIZE

21-SEP-2001; 2001US-0324152P.
25-SEP-2001; 2001US-0329692P.
25-OCT-2001; 2001US-0339924P.
30-OCT-2001; 2001US-0350973P.
30-OCT-2001; 2001US-0340924P.
18-DEC-2001; 2001US-0341732P.
18-DEC-2001; 2001US-0341776P. 21-SEP-2001; 

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(AFFI-) AFFINIUM PHARM INC

봈 Beattie B; I, Mansoury Vedadi M, Alam MZ, Awrey D, Kanagarajah D, Nethery K, Ng Viola C, Wrezel O; Dharamsi A Houston S. Pinder B, Mcdonald M, Edwards A, Domagala M,

2003-468119/44 WPI; 2003-468119, P-PSDB; ADD15465 Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

SEQ ID NO 29; 325pp; English. Claim 20;

This interior teraces to me structural and interioral characterisation.

Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)

Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)

Chat provide novel antimicrobial targetes. Specifically, it refers to polypeptides that are involved in membrane biosynthesis, which play a critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also fusion proteins. These proteins provide structural and functional confusation to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for developing antimicrobial agents for use as surface disinfectents,

Consideration of the experimentally predicted DNA of S. aureus UDP-Ninvention relates to the structural and functional characterisation acetylmuramate-alanine ligase (murc) of

Sequence 1335 BP; 472 A; 160 C; 255 G; 448 T; 0 U; 0 Other;

120 141 180 201 240 261 300 321 9 8 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC Gарв .. DB 9; Length 1335; 1; Indels Score 1263; DB; Pred. No. 0; Mismatches Query Match
Best Local Similarity 99.9%;
Matches 1313; Conservative 82 121 142 181 241 à 셤 ð d Š 셤 à d à

1020 1101 1200 1221 1260 1281 009 099 681 720 840 960 981 480 621 741 780 900 381 420 441 501 561 801 861 921 ATTIGCTTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 982 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTTCAAATTACGGATAAAGGT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTTAGAGAAGCTA GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGGTTAAAACGTCGTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT CAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1042 CAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 102 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA CATGTTATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT rrecercaaagrearrarrrecerrrreagecarergaararagacercaerrraagr GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ACTIGCTTTTGATGTGTATGTGGTGAGGTTTTTATGATCACTTCCTGTCTCCACAATAT ACTGCTTTTGATGTGTGTGGTGAGTTTTTATGATCACTTCCTGTCTCCACATAT GABACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCCATCCAAGAGAAATT 1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTTGGATCAATTAGAGAAAATACTGGCGCA CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314 1282 CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1335 322 442 601 661 721 742 802 841 862 922 961 1162 1261 781 1021 1141 382 502 541 562 622 682 901 301 421 481 심 셤 셤 à g ð 셤 à 유 à 셤 ò 셤 Š 셤 Š 셤 Š 셤 à 엄 ઠે ò à 셤 ઠ d à 셤

ACA19726 standard; DNA; 1314 BP ACA19726 ID ACA:

(ELIT-) ELITRA PHARM INC. 06-MAR-2002; 

ds; prokaryotic essential gene; cell proliferation; Prokaryotic essential gene #1383 21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-00072851. 21-MAR-2002; 2002WO-US009107 (first entry) Staphylococcus aureus drug design; gene. WO200277183-A2 19-JUN-2003 03-OCT-2002 Antisense; ACA19726

Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C. Malone Zamudio C, Trawick JD; 'n, Wang Wall

2002US-0362699P

WPI; 2003-029926/02 P-PSDB; ABU15856.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 7596; 1766pp; English.

the inventor tradece to an isolated nucleic acta comprising any one or the inventor tradece by an interest specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid confidence operably linked to the nucleic acid confidence operably linked to the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated conflowed and propertied for interest and isolated confidence or its fragment whose expression is inhibited by the antisense nucleic acid, (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an influence of the activity; (11) a culture comprising strains in which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the compound collection of strains; or (13) identifying the target of a compound that inhibits collection of strains; or (13) identifying the target of a compound that inhibits or sereening for homologous nucleic acids are useful for collectional and all and all and all and antisence moleic acids are useful or an organism. The antisence moleic acids are useful for collection of an organism. The antisence moleic acids are useful for collections or screening for nondivernal acids are useful. drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at one of invention relates to an isolated nucleic acid comprising ftp.wipo.int/pub/published_pct_sequences

Sequence 1314 BP; 464 A; 161 C; 250 G; 439 T; 0 U; 0 Other;

92.0%; Score 1212; DB 7;

Query Match

Length 1314;

0 1020 120 120 1080 240 240 300 300 360 360 420 420 480 480 540 540 009 009 099 099 720 720 780 780 840 840 900 960 9 900 960 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA Argentariangeacarcangeactreangearcearantengeactreangeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeacarantengeaca GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICIACAACAGGITIAITAICA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAACTTCTACAACAGGTTTATTATCA Argacacacraritaricaricasaarraaagerrcregcargagrrcarragcacacaarc GTTGCTCTTAGAAATAAGGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA 361 CATGTTATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA 481 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA CATGTTATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTAAGT 421 TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT ACTGCTTTTGATGTGTTGTGGTGTTTTTTGATCACTTCCTGTCTCCACAATAT CAACCACACATTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT GGTGACCATACAGTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAAACGTCGTTTCAAT GAAACTACAAATTGCAAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT Gaps GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGAAATT 961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT ÷ 2; Indels 0; Mismatches Pred. No. 99.88; Matches 1312; Conservative Best Local Similarity 61 121 121 181 241 301 241 301 601 601 721 196 1021 361 421 481 541 541 661 661 721 781 781 841 901 901 d Š 셤 ਨੋ 셤 ð 임 셤 à 셤 à à g ò d Вb ò ਨੋ g à g 원 8 셤 à ઠે 셤 à 유 셤 셤 8 ଚ à

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                                                       1081 AAAGCAGATCGTGTATTCTTATGTGAAAATTTTTGGATCAATTAGAGAAAAATACTGGCGCA
                                                                                                                                                                       ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTATGGGTGCAGGTGATATT
                                  1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                                                     1201 ATTAATGTATTAGAACAATTTGATAATGCTGTTGTTTTTATTGGGTGCAGGTGATATT
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                                                                                                                                                                                                                                      CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cellular proliferation gene; antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Staphylococcus aureus DNA for cellular proliferation protein #870.
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
                                                                                                                                                                                                                                                                                                                                                            AAS54558 standard; DNA; 1335
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2001US-0269308P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; ds; prokaryotic
antibacterial, drug design
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Xu HH;
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia soli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonae aeruginosa and Entercoccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can antibodies care compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids. Claim 27; SEQ ID NO 8195; 511pp; English

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WPI; 2001-611495/70. P-PSDB; AAU35699.

ö nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences 120 141 180 201 240 261 300 321 360 420 480 540 381 441 501 900 99 561 621 681 720 741 780 840 9 801 921 81 202 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 262 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA 1 ATGACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 22 Argacacrarcarrirgreggaarraaaggreggegregggreggerrearraggacacaaare 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 82 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 121 GITGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACATAAAAGAA 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 241 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA 142 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGGTGCTAATAACATAAAAGAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA GGTGACCATACAGTITITAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAAACGTCTTTCAAT CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TIGCCIGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT Trigocrigaaagrigarrarracecrirrigaegearergaararagaegreerrrrraagr TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTCAAA **ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT** ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAC TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT **ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT** 742 ACTGCTTTTGATGTGTGTGGATGGTGATTTTATGATCACTTCCTGTCTCCACAATAT GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGGTTAAACGTCGTTTCAAT Gaps ; 0 Length 1335; Sequence 1335 BP; 472 A; 164 C; 255 G; 444 T; 0 U; 0 Other; Indels 7; 72.6%; Score 957; DB 4; 99.5%; Pred. No. 0; 0; Mismatches Best_Local Similarity 99.5 Matches 1307; Conservative 301 361 382 442 502 562 601 622 682 Query Match 421 481 841 541 661 721 802 781 88888888 ਨੇ ద ò 吕 Ś 엄 à à 원 δ 셤 심 ò 셤 ठ ద δ 셤 à ద ð ద à 유 ò 셤 셤 ठे 8

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AAS51660 ID AAS51660 standard; DNA; 1311 BP. XX AC AAS51660; XX DT 13-FEB-2002 (first entry) XX XX DE Staphylococcus aureus DNA for cellular proliferation protein #77.

RESULT 7

Antisense, ds, prokaryotic cellular proliferation gene, antibiotic, antibacterial; drug design.

Staphylococcus aureus. WO200170955-A2. 27-SEP-2001.

21-MAR-2001; 2001WO-US009180

21-MAR-2000, 2000US-0191078P.
23-MAY-2000; 2000US-0206848P.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0253625P.
27-NOV-2000; 2000US-0253625P.
25-DEC-2000; 2000US-0253625P.

(ELIT-) ELITRA PHARM INC.

Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ; Yamamoto RT, Xu HH; WPI; 2001-611495/70.

P-PSDB; AAU33801. New polynucleotides for the identification and development

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Claim 27; SEQ ID NO 4242; 511pp; English.

antibiotics, comprise sequences of antisense nucleic acids

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes,

their use in the discovery of novel antibiotics, the essential genes
themselves and the encoded proteins. The prokaryotes used are Escherichia
coli, Staphylococcus aureus, Salmonella typhi, Rlebsiella pneumoniae,
Pseudomonas aeruginosa and Esterococcus faccalis. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense nucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
be used to screen compounds in rational drug discovery programmes. The
antisense nucleic acids equence is also useful to screen for homologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence encodes an essential prokaryotic
cellular proliferation protein. Note: The sequence data for this patent
did not form part of the printed specification, but was obtained in
electronic format directly from WIDO at
tp. wipo.int/pub/published_pot_sequences ó 120 240 240 099 780 120 180 180 300 300 360 420 540 540 900 099 720 360 420 480 480 009 720 09 9 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 121 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGGTGCTAATAACATAAAGAA 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 241 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA TATAAACCTGATTACGCAATTATGACAAATATTGGATTTCGATCATCCTGATTATTCAAA ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAC 721 ACTGCTTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT 1 Argacacaciarcarrirgressaarraaassrrersscarsastrearrascacaaare ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA GTTGCTCTTAGAAATAAGGGGGATAAAATATTACCATTTGATGCTAATAACATAAAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATGITATGAATGGTGATAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA CATGITATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TIGCCIGAAAGIGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT ATTGCTTGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT 661 TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT Gарв . 0 4; Length 1311; Sequence 1311 BP; 462 A; 164 C; 250 G; 435 T; 0 U; 0 Other; 7; Indels Score 954; DB 4; Pred. No. 0; 0; Mismatches Query Match 72.4%; Best Local Similarity 99.5%; Matches 1304; Conservative 61 121 181 241 301 301 361 361 421 421 481 481 541 541 601 601 661 8 셤 셤 엄 g 유 ДQ ò 셤 g ð ద à d 8 셤 8 셤 à ò à ò Š à à

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/gene= "Murc"
/product= "UDP-N-acetylmuramate:L-alanine ligase (MurC
polypeptide)"
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                                                 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAAAGCTA
                                                                           GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGATTAAACGTCGTTTCAAT
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                                                                                                                                                                                                                                                                                                                               UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA.
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The present sequence represents a MurC gene encoding a Staphylococcus aureus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell contraining an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for confection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising cutibodies, to identify modularors or specific receptors; in rational days or influence and as an immunogen for vaccines. The Murc gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant Murc gene; in influence or influence and for genetic influences and influences and influences are influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences and influences
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Best Local Similarity 99.6%;
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                                               WPI; 1999-062655/06.
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Staphylococcus aureus contig SEQ ID #392

(first entry)

16-MAR-1999

AAV74703;

Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

Staphylococcus aureus.

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence" Location/Qualifiers 1141. 1200 /*tag= Key misc_feature

96US-0009861P (HUMA-) HUMAN GENOME SCI INC 97EP-0010011 07-JAN-1997; 05-JAN-1996; EP786519-A2. 30-JUL-1997 AAV74703
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Rosen CA; Fannon MR, Dillon PJ, Barash SC, Choi GH, ð Kunsch

GATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAATTGAAG

1741

WPI; 1997-374922/35

:leotide(s) and proteins derived from Staphylococcus aureus -on computer readable medium and used in the production of anti-Polymucleotide(s) and .aureus vaccines.

Claim 1; Page 1287-1288; 3271pp; English.

This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows buttaive functions to be assigned so industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can lake be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can be used the meanly meanly are useful as primers or probes for isolating head-allow meanly. readable

Sequence 2424 BP; 839 A; 302 C; 462 G; 759 T; 0 U; 62 Other;

1320 0; 1560 694 GATCAATTAGAGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAG 934 TGGCACATAATGTTAAAAAAGGTATTATTGCTTGGGGTGATGATGAACATCTACGTAAAA AAAATATTCAAATTACGGATAAAGGTACTGCTTTTGATGTGTATGTGGATGGTGAGTTTT TTGAAGCAGATGTTCCAATTTATTATTGATTTAAAGATTCGGATGACATTTATGCTC 695 AAAATATTCAAATTACGGATAAAGGTACTGCTTTTGATGTGTATGTGGATGGTGAGTTTT 755 ATGATCACTTCCTGTCTCCACAATATGGTGACCATACAGTTTTAAATGCATTAGCTGTAA 1441 TTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGT TTGGTGGTGTTAAACGTCGTTTCAATGAAACTACAATTGCAAATCAAGTTATTGTAGATG CACATAAAGAAGTTGTTGCAGTATTTCAACACACACACTTTCTCTAGAACACAGGCATTTT TTGAAGCAGATGTTCCAATTTATTATGGATTTAAAGATTCGGATGACATTTATGCTC TTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGT CACATAAAGAAGTIGTIGCAGTATTICAACCACACACTTICTCTAGAACACAGGCATTTT TAAATGAATTTGCAGAAAGTTTAAGTAAAGCAGATCGTGTATTCTTATGTGAAATTTTTG Gaps . 0 DB 2; Length 2424; 0; 0; Indels 100.0%; Preq. w. Score 740; Pred. No. 56.1%; Matches 740; Conservative Local Similarity 635 1321 575 1261 815 875 Query Match 1621 935 995 1055 1115

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Gaps

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120 845

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98/

121 CCATACAGITITIAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGT 846 TACAAATATTAAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTACAATGAAAC 181 TACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAATGAAAC 906 TACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATTAGTGC

CCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGT

666 ATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGC 1 ATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGTACTGC TTTTGATGTGTATGTGGATGGTGAGTTTTATGATCACTTCCTGTCTCCACAATATGGTGA

25.0%; Score 330; DB 2; Length 660; 99.7%; Pred. No. 2.3e-142; ive 0; Mismatches 1; Indels

Matches 380; Conservative

Similarity

Query Match

SKKS

immunisation. The present sequence represents a partial nucleotide sequence (Murc ORF) of the Murc gene

Sequence 660 BP; 233 A; 83 C; 120 G; 224 T; 0 U;

905 240 965

Mon Jun

The invention relates to a UDD-N-acetylmuramate:L-alanine ligase (Murc polypeptide) encoded by the S. aureus Murc gene. Host cells containing an expression system comprising the Murc gene can be used for the ceptression system comparising the Murc gene can be used for the creombinant production of the polypeptide. Agonists or the Murc polypeptide are used to treat conditions requiring increased activity or competitive polypeptide are useful for inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide acid or competitive polypeptide are useful for inhibiting the polypeptide acid or bacterial (especially S. aureus) infections. They are also useful against the intibacterial agants are useful to treat in-dwelling devices for The antibacterial agants are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The Murc polypeptide is also useful for of bacteria to matrix proteins. The Murc polypeptide is also useful for antibodies; to identify modulators or specific receptors; in rational cuseful in antisense/ribozyme therapeutics; to detect mutant Murc gene; for chromosomal mapping; to determine bacterial serotype; and for genetic 1801 GIGCATCGTTAATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTA 1860 1861 ITTTATTTATGGGGGGGGGATGATTCAAAATTACAAAATGCATATTTAGATAAATTAG 1920 New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial GTGCATCGTTAATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTA TTTTATTTATGGGTGCAGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAG Partial nucleotide sequence of the Murc gene. Location/Qualifiers GCATGAAAATGCGTTTTAA 1314 1921 GCATGAAAATGCGTTTTAA 1940 Claim 2; Page 4-5; 39pp; English. (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. AAV80065 standard; DNA; 660 BP 98EP-00305064. 97US-0052720P (first entry) .660 Burnham MKR; Staphylococcus aureus. WPI; 1999-062655/06. P-PSDB; AAW89199 26-JUN-1998; 03-JUL-1997; 17-MAR-1999 EP889123-A2 07-JAN-1999 Wallis NG, infections. 1235 1295 AAV80065; ð g ò g à g

RESULT 11 AAV53479/c ઠે 셤 δ a à a à 유 ò g Murc gene; UDP-N-acetylmuramate:L-alanine ligase; Murc polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation; ds. /*tag= a /product= "partial MurC polypeptide"

TACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACC 1025

996

301

241

TACAAITGACACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACC 360

1026 ACACACTTTCTCTAGAACACA 1046 

Staphylococcus aureus protein; immune response induction; eye infection; antibody production; T-cell immune response; gastrointestinal infection; respiratory infection; inhibitor; bacterial infection; cardiac infection; central nervous system; kidney infection; urinary tract infection; antimicrobial compound identification; broad spectrum antibiotic; DNA encoding a Staphylococcus aureus protein of unknown function. BP. 97EP-00307485. AAV53479 standard; DNA; 619 30-OCT-1998 (first entry) Staphylococcus aureus. therapy; вв. AAV53479;

96US-0027032P. 24-SEP-1997; 24-SEP-1996; 13-MAY-1998, SP841394-A2 

Reichard RW, Nicholas RO; Ward JM, Lonetto MA; Knowles DJC, Rosenberg M, (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC. Hodgson JE, l, Pratt JM, Burnham MKR, Black MT,

WPI; 1998-252940/23. P-PSDB; AAW77686.

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function, and represents a DRA Sequence of the invention. The DNA sequences were isolated from Staphylococcus aureus WGHU29 (NGIMB 40711). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducing an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, particulated, central nervous, eye, kindey, uninary tract, skin, bones and joints. The proteins can also be used to identify antimicrobial compounds which are broad spectrum antibiotics, especially useful in the treatment of H. pylori infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGAAATT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 ACTGCTACAATTGACACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACACCATCCAAGAGAAATT 372
                      - useful in
                  nucleic acid sequences from Staphylococcus aureus WCHU29 - useful innes and for treatment of bacterial infections of e.g. respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Staphylococcus aureus cellular proliferation inhibitory sequence #1575.
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 619;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 619 BP; 208 A; 117 C; 79 G; 215 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                          Score 275; DB 2; L
Pred. No. 6.3e-117;
0; Mismatches 1;
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                                                                                      Claim 1; Page 146; 390pp; English.
                                  vaccines and for treatment of bac
tract and central nervous system
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20.9%;
Best Local Similarity 99.7%;
Matches 325; Conservative (
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Entercoccus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of creaming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of organisms. The present sequence is an antisense oligonuclectide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCATTTGATGCTAATAACATAAAGAAGATATGGTAGTTATACAAGGTAATGCATTCGC 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAGTAGCCATGAAGAAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTATAA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTAGCCATGAAGAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTATAA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGATTITITAGGACAGATTATTGATCAATATACTTCAGTAGCTGTAACTGGTGCACATGG 332
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                                                                                                                                                                                    Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             137 TGATTTTTAGGACAGATTATTGATCATATACTTCAGTAGCTGTAACTGGTGCACATGG
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                                                                                                                                                                                    Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 257; DB 4; Length 257; Pred. No. 1.4e-108;
                                                                                                                                                                                                                                                                         polynucleotides for the identification and development
                                                                                                                                                                                                                                                                                              antibiotics, comprise sequences of antisense nucleic acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 257 BP; 84 A; 50 C; 31 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                  Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Preu. ...
                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 2928; 511pp; English.
                                                                                                                                                                                    Zyskind JW
             23-MAY-2000; 2000US-0206B4BP.
26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-024257BP.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-026931BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.5%;
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ACA17633 standard; DNA; 257
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                                                                                                                                                                                  Ohlsen KL,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 257; Conservative
                                                                                                                                              (ELIȚ-) ELITRA PHARM INC
                                                                                                                                                                                                                                       WPI; 2001-611495/70.
                                                                                                                                                                                Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-0CT-2003
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs. WPI; 2003-029926/02 33-OCT-2002 Archaea. Wang L, Wall D, 

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Antisense; 88; prokaryotic essential gene; cell proliferation;
Prokaryotic essential gene antisense oligonucleotide #5503.
                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2001; 2001US-00948993.
25-007-2001; 2001US-0342923P.
08-EEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362859.
                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                                                          2001US-00815242.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                WO200277183-A2
                                                                                                                                                                                                                                                                                                                                          21-MAR-2001;
                                                                          drug design:
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Zyskind JW; Xu HH; Ohlsen KL, Forsyth RA, Haselbeck R, Yamamoto R, Malone C, Carr GJ, Trawick JD, Zamudio C

Claim 1; SEQ ID NO 5503; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a pronoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting callular or proliferation or the activity of a gene in an operon required for proliferation or that has an activity against a biological pathway contained for proliferation, (7) identifying a compound that influences the activity of required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an identifying agence for cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the strains is present in a culture or collection of a trains; or (13) identifying the target of a compound that inhibits the extent of a trains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleid are useful for a proliferation of an organism. The antisense nucleid are useful for proliferation of an organism. The antisense nucleid are useful for proliferation of an organism. The antisense nucleid are useful for proliferation of an organism. proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the 6213 antisense sequences of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the property from Fig. Wipo.int/pub/published pct_sequences. (Updated on 27-OCT-2003 to standardise OS field)

Sequence 257 BP; 84 A; 50 C; 31 G; 92 T; 0 U; 0 Other;

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                 Score 257; DB 7; Length 257;
Pred. No. 1.4e-108;
                                                 0; Indels
Match
19.5%; Score 25%; Do Local Similarity 100.0%; Pred. No. 1.46
Cocal Similarity 100.0%; Mismatches
                                            Matches 257; Conservative
                 Query Match
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153 ACCATTTGATGCTAATAACATAAAGAAGATATGGTAGTTATACAAGGTAATGCATTCGC 212

The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins The prokaryotes used are Escherichia Feudemonas acruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins, and to obtain antibodies capable of binding to the expressed proteins. The programmes. The antisense nucleic acid sequence is also useful to screen for homologous 332 GAGTAGCCATGAAGAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTTATAA 138 TAAAACTICTACAACAGGTITATIATCACAIGTTAIGAAIGGIGATAAAAAGACTICAIT 392 TAAAACTICTACAACAGGTTTATTATCACATGTTATGAATGGTGATAAAAAGACTTCATT 18 TGATITITIAGGACAGATTATTGATCAATATACTTCAGTAGCTGTAACTGGTGCACATGG 78 TGATTTTTAGGACAGATTATTGATCAATATACTTCAGTAGCTGTAACTGGTGCACATGG Staphylococcus aureus cellular proliferation inhibitory sequence #246. GAGTAGCCATGAAGAAATAGTACGTGCACATCAATTGAAATTAGATGTTGTAAGTTATAA Carr GJ; Antisense; ss; prokaryotic cellular proliferation; antibiotic; Trawick JD, New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids. Zyskind JW, Wall D, Claim 1; SEQ ID NO 1599; 511pp; English. AAS49022 standard; DNA; 225 BP. TITAATIGGIGAIGGCA 409 2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P. 2000US-0257931P. 21-MAR-2001; 2001WO-US009180. rrraarregreareeca 1 2000US-0191078P. drug design. 13-FEB-2002 (first entry) (ELIT-) ELITRA PHARM INC Haselbeck R, Ohlsen KL Yamamoto RT, Xu HH; Staphylococcus aureus. WPI; 2001-611495/70 antibacterial; WO200170955-A2 21-MAR-2000; 22-DEC-2000; 16-FEB-2001; 23-OCT-2000; 27-NOV-2000; 26-MAY-2000; 27-SEP-2001 23-MAY-2000 257 213 197 273 137 333 77 17 AAS49022; 393 RESULT 14 AAS49022, g 셤 셤 ò 용 ⋩ ò ઠ 셤 

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nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligomuclectide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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prokaryotic cellular proliferation, their use in identifying the genes,
their use in the discovery of novel antibiotics, the essential genes
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                                                                                         Sequence 225 BP; 79 A; 44 C; 31 G; 71 T; 0 U; 0 Other;
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16-FEB-2001; 2001US-0269308P.
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26-MAY-2000;
23-OCT-2000;
27-NOV-2000;
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themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonalla typhi, Klebsiella pneumoniae, Pseudomonae aeruginosa and Enterococcus faecalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of from WIPO at ftp.wipo.int/pub/published_pot_sequences
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-712-713-1 1318 Perfect score: Title:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Aas00189 S. aureus	Add15462 Staphyloc	Add15464 Staphyloc	Acf72770 Staphyloc	Aca19726 Prokaryot	Aas54558 Staphyloc	Aas51660 Staphyloc	Aav99650 UDP-N-ace	Aav74703 Staphyloc	Abn92833 Staphyloc	Aca47124 Prokaryot	Aav80065 Partial n	Aca22277 Prokaryot	Aav53479 DNA encod	Aas53136 Enterococ	Aca33252 Prokaryot	Continuation (17 o	Abg67195 Listeria	Continuation (2 of	Aca36934 Prokaryot	Continuation (17 o	Aca33597 Prokaryot	Aca47261 Prokaryot
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## ALIGNMENTS

AAS00189 standard; DNA; 1318 BP.

AAS00189;

(first entry) 04-JUL-2001 S. aureus DNA encoding UDP-N-acetylmuramate:L-alanine ligase, MurC.

UDP-N-acetylmuramate:L-alanine ligase; MurC; immunogen; vaccine; antibody; wound infection; cellulitis; burn infection; eyelid infection; food poisoning; joint infection; neonatal conjunctivitis; osteomyellitis; skin infection; scalded skin syndrome; toxic epidermal necrosis; Ritter's disease; Lyell's disease; toxic shock syndrome; endocarditis; 

Staphylococcus aureus.

Location/Qualifiers
1. .1314
/*tag= a
/product= "MurC" Key

WO200116292-A2

08-MAR-2001.

31-AUG-2000; 2000WO-US023773. 99US-0151933P 01-SEP-1999;

(HUMA-) HUMAN GENOME SCI INC.

Choi GH;

WPI; 2001-183259/18. P-PSDB; AAU00828 New isolated nucleic acid for use in diagnosing Staphylococcus infections and in vaccines for eliciting immune responses to the infections.

Claim 1; Page 14; 225pp; English.

The sequence encodes S. aureus MurC (UDP-N-acetylmuramate:L-alanine ligase). The polynucleotides of the invention are used to detect

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Location/Qualifiers
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25-SEP-2001;
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Staphylococcus nucleic acids in a biological sample from an animal for diagnosing Staphylococcus infections. The polypeptides of the invention are used to detect anti-Staphylococcus infections. The polypeptides from an animal to diagnose Staphylococcus infections. The polypeptides are also used in vaccines to elicit protective antibodies in an animal to a member of the Staphylococcus genus and for preventing or attenuating an infection caused by a member of the Staphylococcus genus e.g wound infection caused by a member of the Staphylococcus genus e.g wound infection, cellulitis, burn infection, eyelid infection, food poisoning, confection, and infection, neonatal conjunctivitis, osteomyelitis, skin infection, scalded skin syndrome (also known as toxic epidermal necrosis, Ritter's disease and Lyell's disease), toxic shock syndrome and endocarditis. The polymolocides may also be used in vaccines and for preventing or attenuating a Staphylococcus infection. Antibodies to the polypeptides may be used to purify, detect and target the polypeptides in in vitro and in vivo diagnostic and therapeutic methods
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                                                                                                                                                                                                                                                    100.0%; Score 1318; DB 4;
100.0%; Pred. No. 2.7e-249;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 1318; Conservative
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1080 1020 1080 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTTTATGGGTGCAGGTGATATT 1260 840 1318 1318 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GAAACTACAATTGCAAATGAGTATTGTAGAGTGATTATGCACACATCCAAGAGAATT 961 AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA AAAGCAGATCGTGTATTCTTATGTGAAATTTTTTGAATCAATTAGAGAAAATACTGGCGCA GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAAACGTCGTTTCAAT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCATCCAAGAGAAATT AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT CAACCACACACTTTCTCTTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAGT 1021 CAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTGCAGAAAGTTTAAAGT CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAAGCTT CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTTAAGCTT microbial; antimicrobial; membrane biosynthesis; pathogenic; immunological response; vaccination; surface disinfectant; personal hygiene application; food preservative; ds; gene; murC; UDP-N-acetylmuramate-alanine ligase. Staphylococcus aureus murC DNA (SeqID 27). "Murc protein"

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18-DEC-2001; 2001US-0341732P.
18-DEC-2001; 2001US-0341776P.
19-DEC-2001; 2001US-0341949P.
                (AFFI-) AFFINIUM PHARM INC
                        Dharamsi A,
Houston S,
Pinder B,
                                         WPI; 2003-468119/44.
P-PSDB; ADD15463.
                        Edwards A,
Domagala M,
Mcdonald M,
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Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.

Vedadi M, Alam MZ, Awrey D, Beattie B; Kanagarajah D, Nethery K, Ng I, Mansoury K; Viola C, Wrezel O;

Claim 20; SEQ ID NO 27; 325pp; English.

This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus), Streptococcus preumoniae (S. pneumoniae) and Sacherichia coli (E. coli) that provide novel antimicrobial targets. Specifically, it refers to critical role in the life cycle and viability of their pathogenic species of critical role in the life cycle and viability of their pathogenic species of origin, and hence provide valuable drug targets. Furthermore, the invention describes modified version of these proteins that facilitate characterisation by labelling with isotopic or heavy atoms, and also fusion proteins. These proteins provide structural and functional information to aid the discovery of therapeutic molecules to treat disorders associated with a particular pathogenic species. As such, they are useful for inducing an immunological response in an individual and as an antigen for vaccination purposes. The polypeptides are also useful for develophing antimicrobial agents for use as surface disinfectants, personal hygiene applications and as food preservatives or in treating for sequence is DNA predicted from the genomic sequence of S. aureus UDP-Nacetylmuramate-alanine ligase (murc) of the invention,

Sequence 1335 BP; 472 A; 161 C; 255 G; 447 T; 0 U; 0 Other;

180 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120 AIGCAIGAITIAGGACAIGAAGITCAAGGAICGGAIATIGAGAACIACGAITITACAGAA 141 201 240 261 300 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTTAGGACAGATTATTGAATGATGA 321 360 TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAACTTCTACAAAGAGGTTTATTATCA 381 420 9 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAGAA CATGTTATGAATGGTGATAAAAGACTTCATTTTAATTGGTGATGGCACAGGTATGGGA 1 AIGACACACTATCATTITGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAACTGGTGCACATGGTAAAACTTCTACAACAGGTTTATTATCA Gaps GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA . . Length 1335; Query Match

99.7%; Score 1314; DB 9; Length 1.
Best Local Similarity 100.0%; Pred. No. 1.6e-248;
Matches 1314; Conservative 0; Mismatches 0; Indels 121 142 181 202 241 262 301 361 322

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ඊ <u>සි</u>	421 TTGCC               442 TTGCC	CTGAAAGTGATTATTTGGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT 	501
8 5	481 TATAAAC	ACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTCGATATTTAAA	r) i
à		TAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT	1009
q	 562 GATAT	GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAGGTATT	62
à	601 ATTGC	TTGGGGGTGATGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT	099
셤	622 ATTGC	ATTGCTTGGGGTGATGAAGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT	681
8		TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT	
d D	N	atttaaagattoggatgacatttatgctcaaatattcaaattacggataaaggt	7
ò	721 ACTGC	ACTGCTTTTGATGTGTGGATGGTGAGTTTTTATGATCACTTCCTGTCTCCACAATAT	780
අ	742 ACTGC	TTTTGATGTGTATGTGGATGGTGATTTTATGATCACTTCCTGTCTCCCCACAATAT	801
ඊ සි	781 GGTGA       802 GGTGA	GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA	840
à			0
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ò	901 GAAAC		96
qq	922 GAAAC		981
ò	961 AGTGC		1020
<del>Q</del>	982 AGTGC	AGTGCTACAATTGAAACAGCACGAAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT	1041
à	1021 CAACC		1080
qq	1042 CAACC	CAACCACACTITCICTAGAACACAGGCATITITAAATGAATITGCAGAAAGITITAAGT	1101
λŏ	1081 AAAGC		1140
ф	1102 AAAGC		1161
ò	1141 TTAACC		1200
qq	1162 TTAACC		1221
ð	1201 ATTAA1	ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTATTTA	1260
q	1222 ATTAAT		1281
à	1261 CAAAAA	AITACAAAATGCATATTTAGATAAATTAGGCATGAAAAATGCGTTTTAA 1314	
qq	1282 CAAAAA		
RESULT ADD1546 ID AD	3 4 D15464	ard; DNA; 1335 BP.	
ž ž	D15464;		
<b>4</b> E 3	-JAN-2004 (1	irst er	
<b>18</b> 3	aphylococcus	aureu	
<b>E</b> E	microbial; anti immunological r	microbial, antimicrobial; membrane biosynthesis; pathogenic; immunological response; vaccination; surface disinfectant;	

**ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA** 

82

300

321

360

420 441 480

501

540

561

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This invention relates to the structural and functional characterisation of microbial polypeptides from Staphylococcus aureus (S. aureus),

Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)

that provide novel antimicrobial targets. Specifically, it refers to

that provide novel antimicrobial targets. Specifically, it refers to

colypeptides that are involved in membrane biosynthesis, which play a

critical role in the life cycle and viability of their pathogenic species

colorigin, and hence provide valuable drug targets. Furthermore, the

colorigin, and hence provide valuable drug targets. Furthermore, the

colorigin, and hence provide valuable of these proteins that facilitate

colorigin, and hence provide valuable structural and functional

colorigin. These modified version of these proteins to treat

colorigin proteins. These proteins provide structural and functional

colorigin proteins provide structural and functional

colorigin associated with a particular pathogenic species. As such, they

colorigin antimicrobial agents for use as surface disinfectants,

colorigin antimicrobial agents for use as surface disinfectants,

colorigin antimicrobial and as food preservatives or in treating

colorigin products to eliminate potential pathogens. This polynucleotide

colorigin the experimentally predicted DNA of S. aureus UDP-N-

colorigin and annine ligase (murc) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel crystallized recombinant polypeptides from Staphylococcus aureus, Streptococcus pneumoniae and Escherichia coli and which are involved in membrane biosynthesis, useful as targets for pathogenic bacteria.
personal hygiene application; food preservative; ds; gene; murC; UDP-N-acetylmuramate-alanine ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1335 BP; 472 A; 160 C; 255 G; 448 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vedadi M, Alam MZ, Awrey
Kanagarajah D, Nethery K,
Viola C, Wrezel O;
                                                                                                                              1. .1335
/*tag= a
/product= "MurC protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20; SEQ ID NO 29; 325pp; English.
                                                                                                   Location/Qualifiers
1. .1335
                                                                                                                                                                                                                                                                                                                     21-SEP-2001; 2001US-0323992P.
21-SEP-2001; 2001US-0324152P.
25-SEP-2001; 2001US-0334652P.
26-OCT-2001; 2001US-0339924P.
29-OCT-2001; 2001US-0339924P.
30-OCT-2001; 2001US-0340924P.
18-DEC-2001; 2001US-0341732P.
18-DEC-2001; 2001US-0341776P.
19-DEC-2001; 2001US-0341776P.
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Best Local Similarity 99.9%;
Matches 1313; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AFFI-) AFFINIUM PHARM INC.
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Houston S,
Pinder B,
                                                                Staphylococcus aureus
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Domagala M,
Mcdonald M,
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Beattie B; I, Mansoury K;

D, Ng

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AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA 1161
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                          GTTGCTCTTAGAAATAAGGGGGATAAAAATATTACCATTTGATGCTAATAAAAAGAA
                                                                       GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
                                                                                                GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA
                                                                                                                                               CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTAGGACAGATTATTGATCAA
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ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 141

61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC

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1222 ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTATTATGGGTGCAGGTGATATT 1281
                                                                                                                                                                                                                                                                         Zyskind JW;
Xu HH;
                                                                                                                             prokaryotic essential gene; cell proliferation;
                CAAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTT
                             1282 CAAAATTACAAATGCATATTTAGATAAATTAGGCATGAAAATGCGTTT
                                                                                                                                                                                                                                                                         Ohlsen KL,
Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                               Claim 14; SEQ ID NO 7596; 1766pp; English
                                                                                                              Prokaryotic essential gene #1383
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                                                                                                                                                                                                                                                                        Malone C,
                                                                                                                                                                                                           21-WAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0342292P.
06-WAR-2002; 2002US-0362699P.
                                                                  ACA19726 standard; DNA; 1314
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                                                                                                entry)
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                                                                                                                                                  Staphylococcus aureus
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Trawick JD,
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                                                                                                                                    drug design;
                                                                                               19-JUN-2003
                                                                                                                                                                              03-OCT-2002
                                                                                 ACA19726;
                                                                                                                                                                                                                                                                      Wang L,
Wall D,
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antisense nucleic acids, useful for identifying proteins or screening homologous nucleic acids required for cellular proliferation to atte candidate molecules for rational drug discovery programs.

the 6213 antisense sequences given in the specification where expression of the mucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the mucleic acid enoding a polypeptide whose expression is inhibited by the antisense mucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense mucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits escilular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent of the inhibits in which the gene product is overexpressed or underexpressed; (12) determining the extent of the inhibits in which the gene or inhich and in the properties of the compound the inhibits in which the gene or inhich a proliferation or inderexpenses of the compound the inhibits in which the gene or inhich and in the properties of the compound the inhibits in which the gene or inhich and in the properties of the compound the inhibits in the extent the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the compound the to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antiseense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids The invention relates to an isolated nucleic acid comprising any one

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required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aernginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                        Length 1314;
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                                                                                                         Sequence 1314 BP; 464 A; 161 C; 250 G; 439 T; 0 U; 0 Other;
                                                                                                                           0; Mismatches
                                                                                                                                        99.54;
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Matches 1312; Conservative
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their use in the discovery of novel antibiotics, the essential genes
themselves and the encoded proteins. The prokaryotes used are Escherichia
coli, Staphylococcus aureus, Salmonella typhi, Rlebsiella pneumoniae,
Pseudomonas aeruginosa and Esterococcus faceziis. The invention is also
useful for the identification of potential new targets for antibiotic
development. The antisense mucleic acids can also be used to identify
proteins used in proliferation, to express these proteins, and to obtain
antibodies capable of binding to the expressed proteins. The proteins can
catisense nucleic acids sequence is also useful to screen for nomologous
nucleic acids which are required for cell proliferation in a wide variety
of organisms. The present sequence encodes an essential prokaryotic
collular proliferation protein. Note: The sequence data for this patent
did not form part of the printed apecification, but was obtained in
electronic format directly from WIPO at

tp. wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                           Sequence 1335 BP; 472 A; 164 C; 255 G; 444 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                        Score 1302.8; DB 4;
Pred. No. 2.6e-246;
0; Mismatches 7;
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Best Local Similarity 99.5%;
Matches 1307; Conservative
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                                                                         <u> AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT</u>
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2000US-0242578P.
2000US-0253625P.
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Yamamoto RT, Xu HH;
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27-NOV-2000;
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16-FEB-2001;
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ACTGCTTTTGATGTGTATGTGGTGATGTTTTATGATCACTTCCTGTCTCCACAATAT
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Xu HH;
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-025757P.
27-NOV-2000; 2000US-0257591P.
16-FEB-2001; 2001US-0269308P.
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Yamamoto RT,
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Seudomonas aeruginosa and Enterococcus faccalls. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins can be used to screen compounds in rational drug discovery programmes. The nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in clectronic format directly from WIPO at the variety fits. wipo.int/pub/published_pot_sequences
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                                                    New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
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Pred. No. 1e-245;
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                                                                                                                 Claim 27; SEQ ID NO 4242; 511pp; English
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P-PSDB; AAU33801.
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/*tag= a /gene= "Murc" /product= "UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide)" UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoding DNA MurC gene; UDP-N-acetylmuramate:L-alanine ligase; MurC polypeptide; bacterial; infection; H. pylori; cancer; ulcer; gastritis; vaccine; immunogen; drug; genetic immunisation; ds. Location/Qualifiers AAV99650 standard; DNA; 1351 BP (first entry) .1335 Staphylococcus aureus. 17-MAR-1999 AAV99650 RESULT 8 Key 

The present sequence represents a MurC gene encoding a Staphylococcus arreaus UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide). Host cell containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (sepecially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising artibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/riboxyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic New isolated MurC polypeptide from Staphylococcus aureus and related nucleic acid - useful in diagnosis, treatment and prevention of bacterial GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA 142 GTTGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGGTGCTAATAACATAAAAA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 1 ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 22 ATGACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC 61 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 82 AIGCAIGAITIAGGACAIGAAGIICAAGGAICGGAIAIIGAGAACIACGIAITIACAGAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA Gaps DB 2; Length 1351; ; Sequence 1351 BP; 471 A; 166 C; 260 G; 454 T; 0 U; 0 Other; 98.1%; Score 1293.2; DB 2; Length larity 99.0%; Pred. No. 2e-244; Conservative 0; Mismatches 13; Indels - 1 Claim 2; Page 3-4; 39pp; English SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC. 97US-0052720P. 98EP-00305064 Wallis NG, Burnham MKR WPI; 1999-062655/06. Best_Local Similarity Matches 1301; Conserv P-PSDB; AAW87771 26-JUN-1998; 03-JUL-1997; 07-JAN-1999 infections. 181 202 121 241 262 Query Match g à 셤 ઠ 셤 à 셤 Š

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EP889123-A2

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cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.

/*tag= a /note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence"

Location/Qualifiers 1141. .1200

misc feature

Staphylococcus aureus

Rosen CA;

Dillon PJ, Fannon MR,

Barash SC,

Choi GH,

Kunsch CA,

WPI; 1997-374922/35

(HUMA-) HUMAN GENOME

97EP-00100117. 96US-0009861P.

07-JAN-1997; 05-JAN-1996;

EP786519-A2 30-JUL-1997 rolynucleotide(s) and proteins derived from Staphylococcus aureus stored on computer readable medium and used in the production of s S.aureus vaccines.

Claim 1; Page 1287-1288; 3271pp; English.

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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The colypeptides can also be used in a kit for the immunodetection of solypeptides can also be used in a kit for the immunodetection of skin and surgical wound infections, scalded skin syndrome, toxic shock of syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences can the computer condition and their fragments are useful as primers or probes for isolating the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the computer and the c
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Computer readable medium; vaccine; S.aureus infection; immunodetection;

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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid encoding a Staphylococcus epidermis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                  Staphylococcus epidermidis ORF nucleic acid sequence SEQ ID NO:2296
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the inventor trainers of the control of a call. Also included are of the mucleic acid inhibits proliferation of a call. Also included are:

(1) a vector comprising a proliferation of a call. Also included are:

(1) a vector comprising a proliferation of a call. Also included are:

(1) a vector comprising a proliferation of a call. Also included are:

(2) a host call containing the vector; (3) an isolated prolypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding callisense nucleic acid; (4) an antibody capable of specifically binding callisense nucleic acid; (4) an antibody capable of specifically binding callisense nucleic acid; (4) an antibody capable of specifically binding colliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for collidar proliferation or the biological pathway required for proliferation, or that inhibits proliferation or the biological pathway required for proliferation or that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene or which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the extent compound's activity; (11) a culture compound that inhibits the compound of an organism. The antisense nucleic acids are useful for confidentifying proteins or screening for homologous nucleic acids required confidentifying the careful confidentifying the capacidate molecules for rational confidentifying the capacidate molecules for rational confidentifying the capacidate molecules for rational confidentifying the capacidate molecules for rational confidentifying the capacidate and confidentifying the capacidate candidate molecules for rational confidentifying the capacidate candidate molecules for rationa
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Xu HH;
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for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                        ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
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                                                                                                                                         Prokaryotic essential gene #28781
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0072851.
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Trawick JD,
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P-PSDB; ABU43254.
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U; 0 Other;

Sequence 1311 BP; 473 A; 181 C; 243 G; 414 T; 0

1260

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The invention relates to a UDP-N-acetylmuramate:L-alanine ligase (MurC polypeptide) encoded by the S. aureus MurC gene. Host cells containing an expression system comprising the MurC gene can be used for the recombinant production of the polypeptide. Agonists or the MurC polypeptide are used to treat conditions requiring increased activity or expression of the polypeptide. Antagonists, inhibitory nucleic acid or competitive polypeptide are useful for inhibiting the polypeptide e.g. bacterial (especially S. aureus) infections. They are also useful against Helicobacter pylori infections and related cancers, ulcers and gastritis. The antibacterial agents are useful to treat in-dwelling devices for
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                                                                   1081 AAGGCAGACCAAGTATTTTTTATGTGAAATATTCGGTTCAATAAAGAGAAATACGGGAGAT
                CAACCACATACGTTCTCAAGAACTCAAGCATTTTTAAACGAATTTGCTGAGAGTTTAAGT
                                            AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Partial nucleotide sequence of the MurC gene
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nucleic acid -
infections.
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                                                           ATGACACACTATCATTTTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC
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                                                                                                                                                                                                                                                                                                 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA
                                 Gaps
                              ;
   Length 1311;
                                Indels
 Score 915.8; DB 7;
Pred. No. 2.2e-170;
); Mismatches 247;
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69.5%;
ilarity 81.2%;
Conservative
                Similarity
   Query Match
Best Local Simi
Matches 1064;
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21-MAR-2001; 2001US-00815242. 06-SEP-2001; 2001US-00948993. 25-OCT-2001; 2001US-0342923P. 08-FEB-2002; 2002US-0072851. 06-MAR-2002; 2002US-0362699P.

(ELIT-) ELITRA PHARM INC

21-MAR-2002; 2002WO-US009107

Bacillus anthracis.

WO200277183-A2 03-OCT-2002

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infection prevention or generally as wound treatments to prevent adhesion of bacteria to matrix proteins. The MurC polypeptide is also useful for diagnosing or prognosing a (susceptibility to) disease, for raising antibodies; to identify modulators or specific receptors; in rational drug design and as an immunogen for vaccines. The MurC gene sequences are useful in antisense/ribozyme therapeutics; to detect mutant MurC gene; for chromosomal mapping; to determine bacterial serotype; and for genetic sequence (MurC ORF) of the MurC gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TTTTGATGTGTGTGTGGATGGTGTTTTATGATCACTTCCTGTCTCCACAATATGGTGA 120
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                                                                                                                                                                                                                                                    48.0%; Score 633; DB 2; Length 660; 98.5%; Pred. No. 6.1e-115; ive 0; Mismatches 10; Indels
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                                                                                                                                                                                                             Sequence 660 BP; 233 A; 83 C; 120 G; 224 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                               639; Conservative
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drug design; gene

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the inversion relates to an interior action where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated or polypeptide; (5) producing the polypeptide; (6) inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation of an pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound we activity; (11) a culture compusion of strains; or (13) identifying at present in a culture or collection of the which each of the strains is present in a culture or collection of proliferation of an organism. The antisense mucleic acids are useful for electrifying proteins or screening for homologous nucleic acids required for electricinal and discovery proverses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or s for homologous nucleic acids required for cellular proliferation isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to an isolated nucleic acid comprising any
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Forsyth RA,
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Pred. No. 5.9e-108;
0; Mismatches 434;
                                                                                                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14; SEQ ID NO 10147; 1766pp; English.
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Carr GJ,
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Best Local Similarity 66.4%;
Matches 858; Conservative
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Trawick JD,
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The DNA sequences were isolated from Staphylococcus aureus WCHU29 (NCIMB 40771). Host cells containing the DNA sequences are used to produce polypeptides or fragments. The proteins are used in the treatment of disease, for inducting an immune response by administering them, to produce antibody and/or T-cell immune response. Antagonists of the proteins are used for the inhibition of bacterial polypeptides. Conditions which may be treated include bacterial infections, especially respiratory, cardiac, and antibodian and proteins are used for the inhibition of bacterial sepecially respiratory, cardiac, and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and an antibodian and antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodian antibodi
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vaccines and for treatment of bacterial infections of e.g. respiratory
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of movel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia chamselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas acruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain attibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The proteins attisense nucleic acids sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent clid not form part of the printed specification, but was obtained in electronic format directly from WIDO at the electronic format directly from WIDO at the printed specification, but was obtained in the process of the printed specification, but was obtained in the process of the printed specification, but was obtained in the process of the printed specification, but was obtained in the process of the printed specification, but was obtained in the process of the printed specification of the printed specification of the printed specification of the printed specification.
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                                                                                        New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1371 BP; 436 A; 236 C; 296 G; 403 T; 0 U; 0 Other;
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Pred. No. 1.4e-99;
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                                                                                                                                                    Claim 27; SEQ ID NO 6773; 511pp; English.
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Best Local Similarity 64.7%;
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26-MAY-2000; 2000US-0207727P.
23-OCT-2000; 2000US-0242578P.
27-NOV-2000; 2000US-0253625P.
22-DEC-2000; 2000US-0257931P.
16-FEB-2001; 2001US-0269308P.
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Xu HH;
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ATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTTCAACCACAC 1029
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                    730 GAIGTGTATGTGGAGTGTTTTATGATCACTTCCTGTCTCCACAATATGGTGACCAT 789
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28 54.4 11.33.3 5.8 4.1 1.8 3.3 5.3 .6 4.1 1.2 3.3 5.3 .6 4.1 1.2 3.3 5.2 .8 4.1 1.2 3.3 5.2 .8 4.1 1.2 3.3 5.2 .8 4.1 1.2 3.3 5.2 .8 4.2 5.2 5.2 3.8 5.2 6.4 4.3 5.2 6.4 5.3 6.4 5.3 6.4 5.3 6.4 5.3 6.4 5.4 5.4 5.4 5.4 5.4 5.4 5.4 5.4 5.4 5	1 1 1 NA SEC-1711 NA APPLIL IN APPLIL IN UNMBE CORRE CORRE TITLE NUMBE CORRE TELEC TELEC TELEC SEQUE SEQUE SEGUE	LENGTH: 2424 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID -08-956-171E-392
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Score 922; DB 4; I
Pred. No. 5.1e-205;
0; Mismatches 245;
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Best Local Similarity 81.4%;
Matches 1069; Conservative
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     Length 2424;
                    Indels
 99.7%; Score 1314; DB 4; L
100.0%; Pred. No. 6.4e-296;
iive 0; Mismatches 0;
Query Match
Best Local Similarity 100.
Matches 1314; Conservative
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AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA
                                                                         ATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTATTTTATGGGTGCAGGTGATATT
                                                                                                                                                                                                                  Sequence 2296. Application US/09134001C

Betant No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn DOUGETCE-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO S

TITLE OF INVENTION: EDIBERADIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 1998-08-13

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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APPLICANT: Pratt, Julie
APPLICANT: Reichard, Richard
APPLICANT: Rosenberg, Martin
APPLICANT: Rosenberg, Martin
APPLICANT: Wand, Judith
TITLE OF INVENTION: Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS: S14
CORRESPONDENCE ADDRESS: ADDRESSE: SMITHKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COUNTRY: USA
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98.0%; Pred. No. 1.6e-123;
live 0; Mismatches 11;
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COMPUTER: IBM Compatible
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
SOFTWARE: FASTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/936,165A
FILING DATE: 24-SEP-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,032
FILING DATE: 24-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: GImmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: PS0549
TELECOMMULICATION INPORMATION:
MENTIONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTAIN TIPE: Diskette MBDIUM TYPE: Diskette COMPUTER: IBM COMPATIBLE
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TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 98.0
Matches 588; Conservative
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TELEX:
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Fatent No. 6348582
GENERAL UNFORMATION:
APPLICANT: Black, Michael
APPLICANT: Burnham, Martin
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Lonetto, Michael
APPLICANT: Lonetto, Michael
APPLICANT: Nicholas, Richard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130 AGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAAGATATGGTA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 TATCATTITATCGGAATTAAGGGATCAGGGATGAGTGCCTTGGCCTTGATGTTGCACCAG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            527
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30.3%; Score 399.2; DB 4; Length 2
Best Local Similarity 59.1%; Pred. No. 1.4e-83;
Matches 759; Conservative 0; Mismatches 513; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FASEISEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/940,572
                                                                                                                                                                                                   APPLICANT: Wallis, Nicola G.
APPLICANT: Black, Michael T.
APPLICANT: Hodgson, John E.
APPLICANT: Knowles, David J.
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Stodola, Robert K.
APPLICANT: Stodola, Robert K.
TITLE OF INVENTION: No. 6310193el Murc
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 08-ULL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P50533-04
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
                                                                                                                                      Sequence 1, Application US/08940572
Patent No. 6310193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2715 base pairs
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MEDIUM TYPE: Diskette
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STRANDEDNESS: double
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                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                           RESULT 5
US-08-940-572-1
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1185 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA 1243
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711 TGTTGCAGTAINTCAAACCACACACTTTCTCTAGAACACAGGCATTTTTAAATGAATTTG 652
                                                                                                                                                                                       591 AGAAAATACTGGCGCATTAACGAWACAAGATTTAATTGATAAAATTGAAGGTGCATCGTT 532
                                                                                                                                                                                                                                                                                                            531 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTCATTTA 472
                                                                                                                                                                                                                                                                                                                                                                                                              471 TGGGTGCAGGTGATATTCAAAATTACAAATGCATATTTAGATAAATTAGGCATGAAAA 412
                                                                                                    651 CAGAAAGITTAAGIAAAGCAGAICGIGIATTICITATTGIGAAATTITTGGATCAATTAG
                                                  1067 CAGAAAGTTTAAGTAAAAGCAGATCGTGTATT--CTTATGTGAAATTTTTGGATCAATTAG
                                                                                                                                                    1125 AGAAAATACTGGCGCATTAACGATACAAGATTTAATTGATAAAATTGAAGTGCATCGTT
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APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Lee, Ving J.
APPLICANT: Martin, Patrick K.
APPLICANT: Martin, Patrick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Los Angeles
STATE: California
CONYTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/265,315
FILING DATE: MATCH 9, 1999
CLASSIFICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATOMERY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/09/265,315
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REGISTRATION NUMBER: 32,327
REFERENCE TOOKET NUMBER: 240/247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 61, Application US/09265315
Patent No. 6187541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
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TELEFAX: (213) 955-0440
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US-09-265-315-61/c
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                                                                                                                                                       APPLICANT: Benton: Bret
APPLICANT: Benton: Bret
APPLICANT: Lee, Ving
APPLICANT: Malouin, Francois
APPLICANT: Malouin, Francois
APPLICANT: Martin, Partick K.
APPLICANT: Schnid, Molly B.
APPLICANT: Schnid, Molly B.
APPLICANT: Schnid, Molly B.
APPLICANT: Schnid: TARET SLAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TITLE OF INVENTION: TARET GENES
NUMBER OF SEQUENCES: 111
CORRESSPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: Salvest Fifth Street
STREET: Sulte 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3; Length 888;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERNENCHOCKET VINBER: 222/005
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: September 13, 1996
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                     Sequence 61, Application US/08714918
Patent No. 6037123
GENERAL INFORMATION:
APPLICANT: Benton, Bret
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 888 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                               US-08-714-918-61/c
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RESULT 9
US-09-266-417-61/c
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                                                                                                                                                                                                                                                                                                                      CAGAAAGITITAAGIAAAGCAGAICGIGIATT--CITAIGIGAAATITITIGGAICAAITAG
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                                                                                                                                                                                 887
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                                                                                                                                                                                                                                                                        828 TTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGGTGA
                                                                                                                                                                                                                                                                                                                                             651 CAGAAAGTTTAAGTAAAGCAGATCGTGTATTTCTTATTGTGAAATTTTTGGATCAATTAG
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                                                                                                                                               Gaps
                                                                                                                                               7;
                                                                                                         29.6%; Score 389.6; DB 3; Length 888; 94.1%; Pred. No. 1.7e-81; ive 1; Mismatches 21; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Benton, Bret
APPLICANT: Lee, Ving J.
APPLICANT: Lee, Ving J.
APPLICANT: Malouin, Prancois
APPLICANT: Malouin, Partick K.
APPLICANT: Mattin, Partick K.
APPLICANT: Schmid, Molly B.
APPLICANT: Schmid, Molly B.
APPLICANT: Sun, Dongxu
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: ARGET GENES
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: ARGET GENES
TITLE OF INVENTION: ARGET GENES
STREET: 633 West Fifth Street
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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US-09-265-315-61/c
; Sequence 61, Application US/09265315
; Patent No. 6187541
LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                       Query Match 29.6
Best Local Similarity 94.1
Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1304 ATGCGTTTTAA 1314
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STATE: California
                                                          linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                    STRANDEDNE

TOPOLOGY:

US-09-265-315-61
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AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA 1243
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                                                                                                                            CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/265,315
FILING DATE: March 9, 1999
CLASSIPICATION: 435
PRIOR APPLICATION 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: 08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 240/247
FELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECO
                                                                 5.0
                                                                 80
COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 888 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 94.1
Matches 462; Conservative
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1185 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTT-ATTTA
                                                                                                                                                                                                                                         531 AATTAATGAAGATTCTATTAATGTATTAGAACAATTTGATAATGTGTTATTTTCATTTA
                                                                         651 CAGAAAGTTTAAGTAAAGCAGATCGTGTATTTCTTATTTGTGAATTTTTTGGATCAATTAG
                                                                                                                  1125 AGRARATACTGGCGCATTAACGATACAAGATTTAATTGATAAATTGAAGGTGCATCGTT
                                                                                                                                                                                                                                                                                                1244 TGGCTGCAGGTGATATTCAAAATTACAAAATGCATATTTAGATAAATTAGGCATGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zun, Dongxu
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS ANTIBACTERIAL
TARGET GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/528,709
FILLING DATE:
PRICATION: 424
PRICA APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 222/005
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SALE 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-528-709-61/c
; Sequence 61, Application US/09528709
; Patent No. 6630303
; GENERAL INFORMATION:
: APPLICANT: Benton, Bret
Lee, Ving
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee, Ving
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
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                                                                                                                                       APPLICANT: Schmid, Molly D.
APPLICANT: Schmid, Molly D.
APPLICANT: Sun, Dongstu
TITLE OF INVENTION: METHODS OF SCREENING FOR COMPOUNDS
TITLE OF INVENTION: ACTIVE ON STAPHYLOCOCCUS AUREUS
TITLE OF INVENTION: TARGET GENES
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 389.6; DB 3; Length
Pred. No. 1.7e-81;
1; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            SIALE: CALLIORIDA
COUNTRY: CALLOIDA
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: B.Crage
COMPUTER: Diskette, 1.44 Mb
MEDIUM TYPE: BCORGETIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPUTER: IBM P.C. DOS 5.0
SOFTWARE: WOLD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/266,417
FILING DATE: MARCH 9, 1999
CLASSIFICATION NUMBER: 08/714,918
APPLICATION NUMBER: 06/009,102
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY/AGENT INFORMATION:
NAME: WAEDLEST RICHARD
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
Sequence 61, Application US/09266417
Patent No. 6228588
                                                           Benton, Bret
Lee, Ving J.
Malouin, Francois
Martin, Patrick K.
Schmid, Molly B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELES: 67-3510
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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94.1%;
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nucleic acid
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Best Local Similarity
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US-09-266-417-61
                                                                                    APPLICANT:
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APPLICANT:
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SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/527,745
FILING DATE: 17-War-2000
CLASSIFICATION: 424
PRIOR APPLICATION DATA: 1996
APPLICATION NUMBER: US/08/714,918
FILING DATE: September 13, 1996
APPLICATION NUMBER: 60/009,102
FILING DATE: December 22, 1995
APPLICATION NUMBER: 60/003,798
FILING DATE: September 15, 1995
ATTORNEY, AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REGISTRATION NUMBER: 32,327
TELECOMPUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
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94.1%;
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                                                                                                                                                                        Gaps
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TARGET GENES
                                                                                                                                                                   21; Indels
                                                                                                                  29.6%; Score 389.6; DB 4 94.1%; Pred. No. 1.7e-81;
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                     TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 61:
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US-09-527-745-61/C
; Sequence 61, Application US/09527745
; Patent No. 6638718
; GENERAL INFORMATION:
; APPLICANT: Benton, Bret
i Malouin, Francois
Malouin, Patrick K. Schmid, Molly B.
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ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette,
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ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth
Suite 4700
STRANDEDNESS: single
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US-09-528-709-61
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                                                                                                                  888 ritragagaagtragarg-rcccaarnrraaagaagcarragaaacg-rrggrggngrraa
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                                                                                                                                                          Gaps
                                        7;
Length 888;
                                                                             TTTAGAGAAGCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTT
                                        Indels
                                        21;
Score 389.6; DB 4;
Pred. No. 1.7e-81;
1; Mismatches 21;
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1016
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
TUTLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockwille
STATE: Maryland
                                                                                                                                                                                                                                                                                       717 AGGTACTGCTTTTGATGTGTATGTGGATGGTGTTTTATGATCACTTCCTGTCTCCACA
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ZIF: 20850
COMPUTER READE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
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US-09-536-784-115
; Sequence 115, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
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                           APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
WUMBER OF SEQUENCE: 452
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                             MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 370.2; DB 3;
Pred. No. 5.9e-77;
0; Mismatches 498;
                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
                                                                                                                 Sciences,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PB340P2
                                                                                 ....urkSEE: Human Genome Scienc STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34(
TELECOMMUNICATION INFORMATION:
TELEFAX: (301) 309-8504
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.1%;
Best Local Similarity 58.6%;
Matches 721; Conservative
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EDNESS: double
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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            GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 370.2; DB 4; Length 1.
Pred. No. 5.9e-77;
0; Mismatches 498; Indels
           SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION NUMBER: 08/961,083
FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHELIE S. MAYKS
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB340P3
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 115:
US-09-536-784-115
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 1267 base pairs
                                                                                                                                                                                                                                                 ELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid_
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                   28.1%;
58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 58.6°
Matches 721; Conservative
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RESULT 14
US-09-107-532A-3260
j Sequence 3260, Application US/09107532A
j Patent No. 6583275
j GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPBUTICS AATTAGTGCTACAATTGAAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGT 1016 961 CTTTCAACCGCATACCTTTACAAGAACCATTGCCTTGTTGGACGACTTTGCCCATGCTTT 1020 1081 regreacerrangeracheaceraceachahareanchahareacheeracerereneer 1140 1141 TGTTGAAAATGTTTCTCCACTCCTAGACCATGACAATGCTGTTTACGTCTTTATGGGAGC 1200 926 900 661 TGGTTCAACCTTCACCGTTCATTTCCGTGGACAAAACTTGGGGGAATTCCACATTCCAAC 841 CACTGAGAAATTGTCAATGATACAGTGATTATCGATGACTTTGCCCACCATCCAACAGA ATATGGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAA 1077 AAGTAAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAG----AGAAAAAAC GCTAGATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTT 781 ATTTGATTTGAACTTGGTGGGGGCACTTGAAAACATTTGCCGGTGTTAAACGTCGTTT TGGCGCATTAACGATACAAGATTTAATTGATAAAAT---TGAAGGTGCATCGTTAATTAA CAATGAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGA 1017 ATTICAACCACACTITCICIAGAACACAGGCATTITIAAAIGAATTIGCAGAAAGITI TGAAGATTCTATTAATGTATTAGAACAATTTGATAATGCTGTTATTTTTATTGGGTGC FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489

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730 GAIGIGIAIGIGGAIGGIGAGIIITAIGAICACIIICCIGICICCACAAIAIGGIGACCAI 789
                                                        757 daidiciarcardegaridaarrigeridegcakricacreraccaecarrederaacae 816
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                                                                                                                                     817 GATATCTTAAAIGCTTTAGGIGTTATTGCAGTAGCTTATGTCGAGAAACTGGATCT 872
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                                                                                                       790 ACAGITITAAAIGCAITAGCIGTAAITGCGATTAGITAITIAGAGAAGCTAGAIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Dechert, Price & Rhoads
: 4000 Bell Atlantic Tower, 1717 Arch Stre
Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FASTEM: DOS SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/940,572 FILLING DATE:
                                                                                                                                                                                                Sequence 3, Application US/08940572

Sequence 3, Application US/08940572

Patent No. 6310193

GENERAL INFORMATION:
APPLICANT: Walls, Nicola G.
APPLICANT: Hodgson, John E.
APPLICANT: Lonetto, Michael T.
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Lonetto, Michael A.
APPLICANT: Stodla, Robert K.
TITLE OF INVENTION: No. 6310193el Murc
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Devi-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024022
FILING DATE: 16-AUG-1996
APPLICATION NUMBER: US 08/889711
FILING DATE: 08-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickingon, Q. Todd
RESISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50533-04
TELECOMMUNICATION INCREATION:
mattername.
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ER: P50533-04
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COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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SEQUENCE CHARACTERISTICS:
LENGTH: 1825 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 215/994-2252
TELEFAX: 215/994-2222
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STRANDEDNESS: double
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US-08-940-572-3/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 GAAAAAGCAAATATCACGATTCTGCCATTTAACGCAGATAATGTAAAACCAGGGATGACG 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 ATCATTGCAĞGAAATGCATTTCCTGATTCACATGAAĞAAATCCAGCĞAĞCAAAAGAATTA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250 AAATTAGATGITGTAAGTTATAATGATTTTTAGGACAGATTATGATCAATATACTTCA 309
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                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...873

; SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

US-09-107-532A-3260
                                                                                                                                                                                                                                                                                                                  ORGANISM: Enterococcus faecium
              TELECOMMUNICATION INFORMATION:
TELEPAX: (781)893-5007
TELEPAX: (781)893-507
INFORMATION FOR SEQ ID NO: 3260:
SEQUENCE CHARACTERISTICS:
LENGTH: 873 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                  TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       535; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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384 GACTICATITITAATIGGIGAIGGCACAGGIAIGGGATIGCCTGAAAGIGATIATITICGC 443

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1498
                                                       CITIGAAICIGACGAAIAIGAGGGICACITCAIGCCITACCACCCAGAAIACICTAITAI 1558
                                                                                                                                                                                        563
                                                                                                                                                  CTTTAACGACTATGCCAAACAAATTACGATGGGTCTTTTTGTCTATGGTGAAGATGCTGA 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                            IGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTAGATGTTACAAATATTAAAGA 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAATTGATAAAAT----TGAAGGTGCATCGTTAATTAATGAAGATTCTATTAATGTATTAG 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 AACAATTIGATAATGCTGTTATTTTTTTTTGGGTGCAGGTGATATTCAAAATTACAAA 1273
                                                                                                                                                                                                                                                                                                                                                                861 AGCATTAGAAACGITTTGGTGGTGTTAAACGTCGTTTCAATGAAACTACAATTGCAAATCA 920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAGCCAATAAAATCAACAAAAAACACCAAGTGÁTTACTGTTGAAAATGTTTCTCCACTCC 838
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                                                                                TITIGAGGCATGTGAATATAGACGTCACTTTTTAAGTTATAAACCTGATTACGCAATTAT
                                                                                                                             564 ATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATTATTGCTTGGGGTGATGAAGA
                                                                                                                                                                         624 TCTACGTAAAATTGAAGCAGATGTTCCAATTTATTATTATGGATTTAAAGATTCGG---A
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Search completed: June 6, 2004, 02:47:06 Job time : 142 secs

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6, 2004, 02:47:10 ; Search time 5352 Seconds
(without alignments)
10673.789 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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1318
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Pred. No. is the number of results predicted by chance to have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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No.	Score	Match	Match Length DB	DB	П	Description
1	1314	99.7	1335	9	AX742069	00000000000000000000000000000000000000
87	1314	99.7	2424	φ	AR354274	12354274 Sequence
E	1311	99.5		9	AX617936	AX617936 Sequence
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c 14	275	20.9	619	ø	AR194630	AR194630 Segment
c 15	90	6.8	888	9	AR149358	AP149358 Sequence
c 16	06	6.8	888	9	AR405068	
c 17	90	6.8	888	9	AR411614	

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Staphylococcus aureus Staphylococcus aureus RESULT 3
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KEYWORDS
SOURCE ORGANISM REFERENCE AUTHORS JOURNAL

Masignani, V.C., Mora, M.C. and Scarselli, W.C. Staphylococcus aureus proteins and nucleic acids Patent: WO 02094868-A 899 28-NOV-2002; Chiron Spa (II) Bacteria; Firmicutes; Bacillales; Staphylococcus

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> > FEATURES

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1102 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTTGGATCAATTAGAGAAAATACTGGCGCA

1081 AAAGCAGATCGTGTATTCTTATGTGAAATTTTTGGATCAATTAGAGAAAATACTGGCGCA

180 1020 141 300 360 420 201 261 381 441 480 501 540 1041 321 561 009 999 621 681 720 741 780 840 801 861 900 921 960 981 GTTGCTCTTAGAAATAAGGGGATAAAATATTACCATTTGATGCTAATAACAAAAAAA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGGGCA GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA TATACTTCAGTAGCTGTAAACTGGTGCAACAAAACTTCTACAACAGGTTTATTATCA CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAGGTATT GATATTAATGATGTTTTTGATGCATTCCAAGAAATGGCACATAATGTTAAAAAAAGGTATT TATGGATTTAAAGATTCGGATGACATTTATGCTCAAAATATTCAAATTACGGATAAAGGT ACTGCTTTTGATGTGTATGTGGTGAGTTTTATGATCACTTCCTGTCTCCACAATAT **ATTGCTTGGGGTGATGAACATCTACGTAAAATTGAAGCAGATGTTCCAATTTATTAT** GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTTAGAGAAGCTA ACTÉCTITIGATGIGIATGIGGAIGGIGAGITITAIGAICACITCCIGICICCACAAIAI GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA GATGITACAATTATAAAGAAGCAITAGAAACGITIGGIGGIGTIAAAACGITITCAAT GATGTTACAAATATTAAAGAAGCATTAGAAACGTTTGGTGGTGTTAAACGTCGTTTCAAT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCACCATCCAAGAGAAATT AGTGCTACAATTGAAACAGCACGAAAGAAATATCCACATAAAGAAGTTGTTGCAGTATTT GAAACTACAATTGCAAATCAAGTTATTGTAGATGATTATGCACCCATCCAAGAAATT CAACCACACATITICITOTAGAACACAGGCATITITAAAITGAATITIGCAGAAAGTITAAGI ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATA 61 82 142 181 202 562 121 241 262 301 322 382 442 502 361 421 481 541 601 199 682 721 742 781 802 841 862 901 922 961 1021

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YQMBVARAQVKSAILPASLFSNDTTVIKELDVSRNHTETMRRHFNIPIEAERLSITTT
PDAIQHIKPADFHVPGDISSARFRIVALITPERDVIHNVGINPTRSGTIDIVEKMG
GNIQLRWOTTGAEPTASTRIQYTPHLQPITIEGELVPRAIDELPVIALLCTQAVGTST
IKDAEELKVKETNRIDTTADMINLLGFELQPTNDGLIIHPSEFKTNATVDSLTDHRIG
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SRVVEIGGIKDKDFYDSETFKANLDRNDVRVIDBSIAQAMRDKIDEAKNEGDSIGGYV
QVVVENNFVGYGSFYNHYDRKLDGKIAQGYVSINAFKGYSFGEGFKAARFOSEIQDEI
LYNSEIGYYRGSNHLGGLEGGMSNGMPIIVNGVMKPIPTLYKPINSVDINTKEDFKAT
IERSDSCAVPAASIVCEHVVAFEIAKALLEEFQSNHIEQLQOQIADRRQINVVEF
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SLAVLFSIVTLPVEFDASSRAMKQITALNIVNEKEYKHARKVLSAAAMTYVAATAVAV
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GDITVNGLVLMFSHSIMAVQAIYFYPRFKRSMIGISVAMIWVFLNDYIDYFHLQFPYY
DFITTHVWQIGVLSCCLSVFGLLYIEINKLLKCK"
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                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (30-JAN-2001) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center, 2Chome 49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan (B-mail:bio@mite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-1333, Fax:81-3-3481-8424)
On Jun 12, 2001 this sequence version replaced gi:13701258.
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NVSKREQRLDDLIVAQLTESFSYQTYLHDKNSMAIDRHKHALLIDYLLHNIDLSLQMN
EKQRFYQLTQILNTIKLVNKRNQFEDIADDD"
Sekimizu, K., Hirakawa, H., Kuhara, S., Goto, S., Yabuzaki, J., Kanehisa, M., Yamashita, A., Oshama, K., Puruya, K., Yoshino, C., Shiba, T., Hattori, M., Ogasawafa, N., Hayash, H. and Hiramatsu, K. Whole genome sequencing of meticillin-resigtant Staphylococcus
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/mol_type="genomic DNA"
/strain="N315"
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Director-General, Biotechnology Ceneer, Aoki, K., Oguchi, A.,
Hosoyama, A., Nagai, Y., Kuroda, M., Hiramatsu, K. and Kikuchi, H.
Direct Submission
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/transl_table=11
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/protein_id="BAB42553.1"
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|db_xref="G1:13701260"
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complement(1578. .2153)
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                                                                                        290638 TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA
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                                                                    TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA
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                              /translation="MKNIISIILGILMFLKLMELLYGAIFLDKPLTKIIFILTLI
YIFYVLVKELIIFLKSKYNKSA"
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/b_xref="d1:13701269"
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PAFVILSSGFGKDEQTSEQTYQVAVALEIJHMATLVHDDVIDKSDKRRGKLTISKKWD
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/transl table=11
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/protein_id="BAB42562.1"
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'protein_id="BAB42560.1"
'db_xref="GI:13701266"
                                                                complement (7597. .7722)
                                                                                                 complement (7597. .7722)
                                                                                                                                                                                                                                                complement (7777. .8226)
                                                                                                                                                                                                                                                                              complement (7777. .8226)
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                                                                                                                                                                                                                                                                                               /gene="ndk"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'gene="gerCC"
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99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="gercc
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Best Local Similarity
Matches 1312; Conserv
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DTLDATIQKKGLLSKRGSRQENYQVLRQTKVPAVLLELGYISNPTDETMIKDQLHRQI
LEQAIVDGLKIYFSA"
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KIYEYFNDALRAYGLTVKTGEFGTHMNVSINNDGPVTIIYESQDGKIQ"
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/transl_table=11
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/db_xref="G1:14247404"
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complement (5654. .6106)
gene="SAV1633"
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/transl_table=11
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protein id="BAB57796.1"
db_xref="GI:14247406"
                               complement (3058. .4320)
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complement(6118. .8307)
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                                                                                                                                                                                                               'note="SAV1631"
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                                                                                     'dene="hiss"
                                                                                                                                                                  gene="hiss"
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         Kuroda,M., Ohta,T., Uchiyama,I., Baba,T., Yuzawa,H., Kobayashi,I.,
Cui,L., Oguchi,A., Aoki,K., Naga,F., Lian,J., Ito,T., Kanamori,M.,
Matsumaru,H., Maruyama,A., Murakami,H., Hosoyama,A.,
Mizutani-Ui,Y., Takahashi,N.K./ Sawano,F., Inoue,R., Kaito,C.,
Sekimizu,K., Hirakawa,H., Kuhara,S., Goto,S., Yabuzaki,J.,
Kanehisa,M., Yamashita,A., Oehima,K., Firuya,K., Yoshino,C.,
Shiba,T., Hattori,M., Ogagwara,N., Hayashi,H. and Hiramatsu,K.
Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (22-FEB-2001) Toshiko Ohta, University of Tsukuba College of Medical Technology and Nursing, Department of Medical Technology, 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan Technology; 1-1-1 Ten-noodai, Tsukuba, Ibaraki 305-8577, Japan Fax:81.298-53-3454, On May 29, 2001 this sequence version replaced gi:13875943.
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DISKTHTDPMAKIIRQKLKKLGIRKGIPVVFSDESPIVIREDVKDIVGDKNAINRKGQ
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/db_xref="taxon:158878"
complement(42..815)
/gene="SAV1628"
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/gene="SAV1629"
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/gene="SAV1628"
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transl_table=11
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TITLE
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                       CATGTTATGAATGGTGATAAAAAGACTTCATTTTTAATTGGTGATGGCACAGGTATGGGA
                                                                                  TTGCCTGAAAGTGATTATTTCGCTTTTGAGGCATGTGAATATAGACGTCACTTTTTAAGT
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IGPRINAVGRLDDASLACELLMTDDEERAAFLAEQVBHFNRERKDIVATITERAMANA
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YRSKRKSLPFTENDBNIVVLIHPKSDRVNANSTYVGERIKQVT
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Dab xref="G1:14247407"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSLQOLQFSQLYIVLQHNHSIYFDGIPNMDIPKKCYKALITKQETNIQKEGMLLCQH
LSVKPDTLKFMLKVFLDLKFVTQEDGLIRINQQPDKRSIDSSKVYQLRQQRMDVEKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                        'note="similar to single-strand DNA-specific exonuclease"
'codon start=1
'transl__table=11
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                          /trans]_table=11
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protein_id="BAB57798.1"
db_xref="GI:14247408"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="protein-export
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                                                                                                                                            complement (9275. .11548)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SAV1637"
/codon_start=1
/transl_table=11
                                                                                                                                                               /gene="SAV1636"
note="SAV1635"
                                                                                                                                 DYDVMSLISYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene="secF"
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Conservative
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Best Local Similarity
Matches 1312; Conserv
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ENIYASQI VYER IRRERERKYLQKRREKKALQQKREEHKNEQDALQRALDEMYAKQA
ERYYGDSSLADDEDLIDNSTDASQLHTNGI ENETVSNDENKQASI QNEDTNDTHVDES
PYNYSENSELNOWYSTYKQLSDDEYTSNYTSOHQSALQHNVENNEDELKNGSRLIADS
BEDGATNKERYSGSQI DDAEFYELNDTRADEDTTSNI EDNTNRANASEMHVDAPKTQEH
AVTESQYNNI DIKTYDNE IELAPRHKKODQTNILAVNSLKTYDVNDGHYVENSSSMNEI EK
HNAEL TENVQNEAABSEQNVERKT I ENVNPKKQTEKVSTLSKRPFNVVMTPSDKKRMM
DRKKHSKYNYPELKRYQSKQAVSESKRASQAAPSSERPSQGESTRYRAYKNMTSNINT
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RIAQKARACGIHMLVATQRESVNVITGLIKANIPELADLAMMAAQGEVEGSIA
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complement (8279. .9136)
                                               SVAVTGAHGKTSTTGLLSHVMNGDKKTSFLIGDGTGMGLPESDYFAFEACEYRRHFLS
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                   NKGIKILPFDANNIKEDMVVIQGNAFASSHEEIVRAHQLKLDVVSYNDFLGQIIDQYT
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QSQDELFDDVCAFMVNEGHISTSLIQRHFQIGYNRAARIIDQLEQLGYVSSANGSKPR
DVYVTEADLNKE"
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VEPTYDENTATAVYXAVDLGKSYRTALIDESMLEDKLATEGO,REMSLENVEKLSNSY
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KTGYDVMAHLTMEFPTKGLVPITSLSPGYKQGHLEPIFILGENNKQKRDPNVIQRLEA
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                                                                                                                                                                                                                                                                                                                                                  /note="DNA translocase stage III sporulation prot homolog
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/codon start=1
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complement(7654. .8250)
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| Ab xref="GI:21204853"
| translation="MTHYHFVGIKGSGMSSLAQIMHDLGHEVQGSDIENYVFTEVALR
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                                                                                                                                                                                                                                                                                                                                                                                                     Director-General, Biotechnology Center, Aoki, K., Oguchi, A., Nagai, Y., Asano, K., Iwama, N., Baba, T., Kuroda, M., Hiramatsu, K. and Kikuchi, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (06-MAR-2002) Director-General, Biotechnology Center, National Institute of Technology and Evaluation, Biotechnology Center, 2Chome 49-10 Nishibara, Shibuya-ku, Tokyo 151-0066, Japan (E-mail:bio@mite.go.jp, URL:http://www.bio.nite.go.jp/, Tel:81-3-3481-8424)
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hypothetical protein, similar to general stress protein
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                                                                                                                      Baba, T., Takeuchi, F., Kuroda, M., Yuzawa, H., Aoki, K., Oguchi Nagai, Y., Iwama, N., Asano, K., Kaima, T., Kuroda, H., Cui, L., Gamanco, K. and Hiramatsu, K. Gamanco, K. and Hiramatsu, K. Genome and will-lance determinants of Migh virulence community-acquired MRSA.
Staphylococcus aureus subsp. aureus MW2
Staphylococcus aureus subsp. aureus MW2
Bacteria; Firmicutes; Bacillales; Staphylococcus.
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YFMNVKGSYIVYEPFVHPETDKYRLVYQGGITTIKNGQNIHYDFYADAYTGEVINIVE
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/product="conserved hypothetical_protein"
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protein_id="BAB95554.1"
/db_xref="GI:21204859"
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/gene="MW1690"
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complement(9612. 10688)
/gene="MW1688"
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                     /note="ORFID:MW1687
thioredoxin homolog"
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NKGIKILPFDANNIKEDMYVIQGNAFASSHEEKARAHQMKLDVVSYNDFLGQIIDQYT
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YKEDYALMTNIDFDHPDYFKDINDVFDAFQEMAHNVKKGIIAMGDBEHLRKIEADVFI
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LEKLDVTNIKEALETFGGVKRRFNETTIANQVIVDDYAHHPREISATIETARKKYPHK
EVVAVFQPHTFSRTQAFLNEFAESLSKADRVFLCEIFGSIRENTGALTIQDLIDKIEG
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Longwood Ave, Boston, MA
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/db_xref="GI:2642659"
                                                                                                                         gene
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/note="MurC; UDP-N-acetylmuramate-alanine ligase"
/codon start=1
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Bacteria; Firmicutes; Bacillales; Staphylococcus.
Lowe, A.B. and Deresiewicz, R.L.
Clowing and sequencing of Staphylococcus aureus messential for cell wall biosynthesis
DNA Seq. 10 (1), 19-23. (1999)
                                                                                                                                                                                                                             Submitted (11-NOV-1997) Channing Laboratory,
Hospital and Harvard Medical School, 181 Long
02115, USA
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/organism="Stapbylococcus aureus"
/wol_type="genomic DNA"
/db_xref="taxon:1280"
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Pred. No. 0;
0; Mismatches 4.
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Lowe, A.M. and Deresiewicz, R.L.
Direct Submission
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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM PLC
OS Unidentified

PN 3D-002300888-A/1

PD 15-OCT-2002

PR 25-DEC-2001

PP 25-DEC-2001

PP 25-DEC-2001

PP 25-DEC-2001

PR 03-JUL-1997 US 60/05279

PI NICOLAG WALLIS, MARTIN K R BURNHAM

PC CIZNI5/09, A61R31/7088, A61R38/43, A61R45/00, A61R48/00,

PC A61P1/00,

PC A61P1/00,

PC A61P3/02, A61P9/08, A61P21/00, A61P13/12, A61P17/00,

PC A61P3/02,

PC A61P3/02, A61P3/00, C07K14/195, C12N1/15, C12N1/19, C12N1/21, PC

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CI2NIS/09, A61K31/7088, A61K38/43, A61K38/55, A61K45/00, A61K48/00, ó 2 E C12P21/02, C12Q1/02, C12Q1/68, G01N33/15, G01N33/50, C12N15/00, PC 180 ATGCATGATTTAGGACATGAAGTTCAAGGATCGGATATTGAGAACTACGTATTTACAGAA 120 141 201 240 261 300 TATACTICAGIAGCIGIAACIGGIGCACAIGGIAAAACTICTACAACAGGIITAITAICA 360 9 81 321 420 480 540 raractricagraderidraecregiecaeargeraaaaerricraeaaeagarriarrarea 381 441 501 561 TTGTCGGAATTAAAGGTTCTGGCATGAGTTCATTAGCACAAATC Argcargattraggacargaagtrcaaggarggarattgagaactacgrattracagaa GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGATGCTAATAACATAAAAGAA 181 GATATGGTAGTTATACAAGGTAATGCATTCGCGAGTAGCCATGAAGAAATAGTACGTGCA 241 CATCAATTGAAATTAGATGTTGTAAGTTATAATGATTTTTTAGGACAGATTATTGATCAA 142 GTTGCTCTTAGAAATAAGGGGATAAAAATATTACCATTTGGTGCTAATAACATAAAGAA Gaps CATGITATGAATGGTGATAAAAGACTICATTTTAATTGGTGATGGCACAGGTATGGGA TIGCCTGAAAGTGATTATTTCGCTTTTGAGGCAIGTGAATATAGACGTCACTTTTTAAGT TATAAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTTAAA 502 TATRAACCTGATTACGCAATTATGACAAATATTGATTTCGATCATCCTGATTATTCAAA TreccieAAAGreArrarrrcecrirrieAGGCATGTGAATATAGACGTCACTTTTTAAGT ., 6; Length 1351; 4; Indels DB Similarity 99.6%; Pred. No. 0; 3; Conservative 0; Mismatches 1. .1351
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644" 1 (bases 1 to 1351) Wallis, N.G. and Burnham, M.K. Location/Qualifiers ATGACACACTATCATT Best Local Simi Matches 1042; 382 442 421 481 g ઠે 쉽 à

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SMITHKLINE BEECHAM CORP, SMITHKLINE BEECHAM CORP FUBLIC LTD CO
OS Unidentified
BN JP 1999225773-A/2
BN 24-AUG-1999
PN 3-JUL-1998 JP 1998225115
PR 03-JUL-1998 JP 1998225115
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CC Strandedness: Double;

CC Topology: Linear;

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PC A61P19/02,A61P19/08,A61P21/00,A61P25/00,A61P27/00,A61P29/00,
PC A61P31/04,
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Pred. No. 5e-217;
0; Mismatches 3; Indels
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/organism='Unidentified'
Location/Qualifiers
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/organism="unidentified"
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ilarity 99.5%;
Conservative (
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1 (bases 1 to 619)
Black, M. Terence., Hodgson, J. Edward., Knowles, D. Justin. Charles., Reichard, R. Winfield., Nicholas, R.O., Burnham, M. Karl. Russel., Pratt, J.M., Rosenberg, M., Ward, J.M. and Lonetto, M. Arthur. Prokaryotic polymuclectides polypeptides and their uses Patent: US 6348582-A 179 A9-FEB-2002;
Location/Qualifiere
                                                                                                                                                                                                                                                                                                                                                                                                                                                 551 GGTGACCATACAGTTTTAAATGCATTAGCTGTAATTGCGATTAGTTATTTAGAGAAGCTA
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                                                                                                                                                                                                                                                                                                                                                                   611 ACTGCTTTTGATGTGTATGTGGTGAGTTTTTATGATCACTTCCTGTCTCCACAATAT
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Benton, B., Lee, V.J., Malouin, F., Martin, P.K., Schmid, M.B.
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Pred. No. 3.5e-133;
0; Mismatches 1;
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                                                                                                                                          1. .619
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6228588.
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/mol_type="unassigned DNA"
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AR149358
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1. .888
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Methods of screening
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Patent: US 6228588-A
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Best Local Similarity 100.0
Matches 90; Conservative
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Best Local Similarity 99.7
Matches 325, Conservative
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PAT 20-APR-2002

linear

Sequence 179 from patent US 6348582. AR194630

GI:20241222

AR194630.1 Unknown. Unknown.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

DEFINITION

Mon Jun 7 10:15:18 2004

DP

507 ATTAGAACAATTTGATAATGCTGTTATTT 478

Search completed: June 6, 2004, 06:04:07 Job time: 5363 Becs